



SEQUENCE LISTING

<110> HIRANO, SEIJI  
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OSUMI, TSUYOSHI  
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SUGIMOTO, SHINICHI

<120> GENES FOR HEAT RESISTANT ENZYMES OF AMINO ACID BIOSYNTHETIC PATHWAY DERIVED FROM THERMOPHILIC CORYNEFORM BACTERIA

<130> 221519US0PCT

<140> 10/089,057

<141> 2002-04-03

<150> PCT/JP00/06913

<151> 2000-10-04

<150> JP 11-282716

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<150> JP 11-311147

<151> 1999-11-01

<150> JP 2000-120687

<151> 2000-04-21

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<170> PatentIn version 3.1

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<221> CDS

<222> (577)..(1869)

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Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp Trp	Asp Thr Asn Pro Arg					
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Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala Glu	Gln Val Ala Glu Leu					
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Gln Gly Ser Val Val Glu Glu His Thr Leu Ala	Lys Arg Gly Ala Glu					
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Ile Leu Trp Asp Ala Val Ser Ala Glu Gly Asp	Asp Tyr Ile Asn Ala					
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ctg ggc gcc ctt acc ggt aac cag gct gtc cag	cag gtc cgt gcc ggc					834
Leu Gly Ala Leu Thr Gly Asn Gln Ala Val	Gln Gln Val Arg Ala Gly					
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ctg aag gct tac ctc tcc ggc tgg cag gtc gca	ggt gac gcc aac					882
Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln Val	Ala Gly Asp Ala Asn					
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Leu Ala Gly His Thr Tyr Pro Asp Gln Ser Leu	Tyr Pro Ala Asn Ser					
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Val Pro Asn Val Val Arg Arg Ile Asn Asn Ala	Leu Leu Arg Ala Asp					
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Glu Ile Ala Arg Val Glu Gly Asp Thr Ser Val	Asp Asn Trp Leu Val					
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Tyr Glu Leu Gln Lys Gly Met Ile Thr Ala Gly	Ala Ala Gly Thr His					
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Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys	Gly His Leu Gly Gly					
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Lys Val Leu Ile Pro Thr Gln Gln His Ile Arg	Thr Leu Asn Ser Ala					
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Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr	Val Val Ile Ala Arg					

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acc gac gca gag gcc	gcc acc ctg atc acc	tct gat gtt gat gag	cgc	1314
Thr Asp Ala Glu Ala	Ala Thr Leu Ile Thr	Ser Asp Val Asp Glu	Arg	
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Asp Arg Pro Phe Ile Thr Gly	Glu Arg Thr Ala Glu	Gly Tyr Tyr His		
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Val Lys Pro Gly Leu Glu Pro	Cys Ile Ala Arg Ala	Lys Ser Tyr Ala		
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Pro Tyr Ala Asp Met Ile Trp	Met Glu Thr Gly	Thr Pro Asp Leu Glu		
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Leu Leu Ser Tyr Asn Cys	Ser Pro Ser Phe Asn	Trp Ser Ala His Leu		
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Glu Ala Asp Glu Ile Ala Lys	Phe Gln Lys Glu Leu	Gly Ala Met Gly		
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Phe Lys Phe Gln Phe Ile Thr	Leu Ala Gly Phe His	Ser Leu Asn Tyr		
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Gly Met Phe Asp Leu Ala	Tyr Gly Tyr Ala Arg	Glu Gly Met Pro Ala		
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ttc gtc gac ctg cag aac cgt	gag ttc aag gca gct	gag gag cgc ggc		1746
Phe Val Asp Leu Gln Asn Arg	Glu Phe Lys Ala Ala	Glu Glu Arg Gly		
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Phe Thr Ala Val Lys His	Gln Arg Glu Val Gly	Ala Gly Tyr Phe Asp		
395	400	405		
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Thr Ile Ala Thr Thr Val Asp	Pro Asn Ser Ser Thr	Thr Ala Leu Lys		
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 Asp Asp Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val  
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 Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile  
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 Ser Asp Val Asp Glu Arg Asp Arg Pro Phe Ile Thr Gly Glu Arg Thr  
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 Ala Glu Gly Tyr Tyr His Val Lys Pro Gly Leu Glu Pro Cys Ile Ala  
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 Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys  
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 Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly  
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 Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala  
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 Val Ser Val Glu Thr Arg  
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 Lys Ile Thr Lys Val Leu Val Ala Asn Arg Gly Glu Ile Ala Ile Arg  
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 Val Phe Arg Ala Ala Arg Asp Glu Gly Ile Ala Ser Val Ala Val Tyr  
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Gly	Thr	Arg	Asp	Cys	Ser	Leu	Gln	Arg	Arg	Phe	Gln	Lys	Leu	Val	Glu		
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Glu	Ala	Pro	Ala	Pro	Phe	Leu	Thr	Asp	Glu	Gln	Arg	Asp	Arg	Ile	His		
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Thr	Val	Glu	Tyr	Leu	Val	Gly	Ser	Asp	Gly	Leu	Ile	Ser	Phe	Leu	Glu		
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Val	Asn	Thr	Arg	Leu	Gln	Val	Glu	His	Pro	Val	Thr	Glu	Glu	Thr	Thr		
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Gly	Ile	Asp	Leu	Val	Arg	Glu	Met	Phe	Arg	Ile	Ala	Glu	Gly	Ala	Glu		
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Leu	Ser	Ile	Lys	Glu	Asp	Pro	Thr	Pro	Arg	Gly	His	Ala	Phe	Glu	Phe		
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Lys	Ile	Thr	Arg	Tyr	Arg	Glu	Pro	Ala	Gly	Pro	Gly	Val	Arg	Met	Asp		
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cgt	tcc	cgt	cgt	gct	ggc	gag	tac	atc	gtc	gag	ggc	atg	ccg	acc	1842		
Arg	Ser	Arg	Arg	Ala	Leu	Gly	Glu	Tyr	Ile	Val	Glu	Gly	Met	Pro	Thr		
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Asp Asn Pro Ile Glu Pro Phe Val Asp Ala Ala Asp Leu Asp Asp Glu	
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Glu Lys Thr Pro Ser Gln Lys Val Ile Val Glu Ile Asp Gly Arg Arg	
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Lys Val Asn Val Glu Asp Gly Ala Glu Val Ser Glu Gly Asp Thr Val	
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Val Val Leu Glu Ala Met Lys Met Glu Asn Pro Val Lys Ala His Lys	
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 Pro Glu Ser Ile Arg Ser Leu Gly Asp Lys Val Thr Ala Arg His Ile  
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 Phe Gln Lys Leu Val Glu Glu Ala Pro Ala Pro Phe Leu Thr Asp Glu  
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 Gln Arg Asp Arg Ile His Ser Ser Ala Lys Ala Ile Cys Arg Glu Ala  
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 Gly Tyr Tyr Gly Ala Gly Thr Val Glu Tyr Leu Val Gly Ser Asp Gly  
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 Leu Ile Ser Phe Leu Glu Val Asn Thr Arg Leu Gln Val Glu His Pro  
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 Val Thr Glu Glu Thr Thr Gly Ile Asp Leu Val Arg Glu Met Phe Arg  
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 Ile Ala Glu Gly Ala Glu Leu Ser Ile Lys Glu Asp Pro Thr Pro Arg  
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 Gly His Ala Phe Glu Phe Arg Ile Asn Gly Glu Asp Ala Gly Ser Asn  
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                   370                  375                  380  
 Gly Gln Phe Asp Ser Met Leu Ala Lys Leu Ile Val Trp Gly Gln Thr  
                   385                  390                  395                  400  
 Arg Glu Gln Ala Leu Glu Arg Ser Arg Arg Ala Leu Gly Glu Tyr Ile  
                   405                  410                  415  
 Val Glu Gly Met Pro Thr Val Ile Pro Phe His Ser His Ile Val Ser  
                   420                  425                  430  
 Asn Pro Ala Phe Val Gly Asp Gly Glu Gly Phe Glu Val Tyr Thr Lys  
                   435                  440                  445  
 Trp Ile Glu Glu Val Trp Asp Asn Pro Ile Glu Pro Phe Val Asp Ala  
                   450                  455                  460  
 Ala Asp Leu Asp Asp Glu Glu Lys Thr Pro Ser Gln Lys Val Ile Val  
                   465                  470                  475                  480  
 Glu Ile Asp Gly Arg Arg Val Glu Val Ala Leu Pro Gly Asp Leu Ala

485	490	495
Leu Gly Gly Gly Ala Gly Ala Ala Lys Lys Lys Pro Lys Lys Arg Arg		
500	505	510
Ala Gly Gly Ala Lys Ala Gly Val Ser Gly Asp Ser Val Ala Ala Pro		
515	520	525
Met Gln Gly Thr Val Ile Lys Val Asn Val Glu Asp Gly Ala Glu Val		
530	535	540
Ser Glu Gly Asp Thr Val Val Val Leu Glu Ala Met Lys Met Glu Asn		
545	550	555
Pro Val Lys Ala His Lys Ser Gly Thr Val Ser Gly Leu Thr Ile Ala		
565	570	575
Ala Gly Glu Gly Val Thr Lys Gly Gln Val Leu Leu Glu Ile Lys		
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<210> 5

<211> 2128

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (339)..(1967)

<400> 5

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cccatacctg cggaaaccac gggaaacacg ggaaaaaccg atctcattca gaccggcgaa	120
atccacactgt ggaacagtca gcggcgccgc catggagggc agcgacaggt gacgtccgag	180
cacccgggttc cccaccgtgg acacggcatt gatccgacac ggtggggata gtttcatgct	240
gaaaaactat cgctgtgcag ggaggatccg gaatgtgacc tatttcatgg agaaatgatt	300
gtggacgata ccccccggta cggctaccat tccaaaac atg acc att tcc tca cct	356
Met Thr Ile Ser Ser Pro	
1	5

ttg att gac gtc gct aac ctg cca gac atc aac acc acc gcc ggc aag	404	
Leu Ile Asp Val Ala Asn Leu Pro Asp Ile Asn Thr Thr Ala Gly Lys		
10	15	20

atc gcc gac ctg aag gcc cgc cgg gcg gaa gcc cac ttc ccc atg ggt	452	
Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu Ala His Phe Pro Met Gly		
25	30	35

gaa aag gcc gta gag aag gtc cac gcg gcc aac cgc ctc acc gcg cgc	500	
Glu Lys Ala Val Glu Lys Val His Ala Ala Asn Arg Leu Thr Ala Arg		
40	45	50

gaa cga ctt gac tac ctg ctc gat gaa ggc tcc ttc atc gaa acc acc gat	548		
Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly Ser Phe Ile Glu Thr Asp			
55	60	65	70

cag ctc gca cgc cac cgc acc acc gcg ttc ggc ctg ggc aac aag cga	596	
Gln Leu Ala Arg His Arg Thr Thr Ala Phe Gly Leu Gly Asn Lys Arg		
75	80	85

ccg gcc acc gac ggc atc gtc acc ggc tgg ggc acc atc gac ggc cgc	644	
Pro Ala Thr Asp Gly Ile Val Thr Gly Trp Gly Thr Ile Asp Gly Arg		
90	95	100

gag gtc tgc atc ttc tcc cag gac ggc acc gtc ttc ggt ggc gca ctc	692
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Glu	Val	Cys	Ile	Phe	Ser	Gln	Asp	Gly	Thr	Val	Phe	Gly	Gly	Ala	Leu	
105												115				
ggt	gag	gtc	tac	ggc	gag	aag	atg	atc	aag	atc	atg	gag	ctg	gcc	atc	740
Gly	Glu	Val	Tyr	Gly	Glu	Lys	Met	Ile	Lys	Ile	Met	Glu	Leu	Ala	Ile	
120												130				
gac	acc	ggc	cgc	cca	ctc	atc	ggc	ctg	tac	gag	ggt	gca	ggt	gcc	cgc	788
Asp	Thr	Gly	Arg	Pro	Leu	Ile	Gly	Leu	Tyr	Glu	Gly	Ala	Gly	Ala	Arg	
135												145			150	
atc	cag	gac	ggt	gcf	gtc	tcc	ctc	gac	ttc	atc	tcc	cag	acc	ttc	tat	836
Ile	Gln	Asp	Gly	Ala	Val	Ser	Leu	Asp	Phe	Ile	Ser	Gln	Thr	Phe	Tyr	
												155			165	
cag	aac	atc	cag	gcc	tcc	ggc	gtg	atc	ccg	cag	atc	tcc	gtg	atc	atg	884
Gln	Asn	Ile	Gln	Ala	Ser	Gly	Val	Ile	Pro	Gln	Ile	Ser	Val	Ile	Met	
												170			180	
ggt	gcc	tgc	gcc	ggt	ggc	aac	gcc	tac	ggc	ccg	gcc	ctg	acc	gac	ttc	932
Gly	Ala	Cys	Ala	Gly	Gly	Asn	Ala	Tyr	Gly	Pro	Ala	Leu	Thr	Asp	Phe	
												185			195	
gtg	gtc	atg	gtg	gac	aag	acc	tcg	aag	atg	ttc	gtc	acc	ggc	ccc	gat	980
Val	Val	Met	Val	Asp	Lys	Thr	Ser	Lys	Met	Phe	Val	Thr	Gly	Pro	Asp	
												200			210	
gtg	atc	aag	acc	gtc	acc	ggc	gag	gag	atc	acc	cag	gag	gag	ctc	ggc	1028
Val	Ile	Lys	Thr	Val	Thr	Gly	Glu	Glu	Ile	Thr	Gln	Glu	Glu	Leu	Gly	
												215			230	
gga	gca	acc	acc	cac	atg	gtc	acc	gcc	ggc	aac	tcc	cac	tac	acc	gtc	1076
Gly	Ala	Thr	Thr	His	Met	Val	Thr	Ala	Gly	Asn	Ser	His	Tyr	Thr	Val	
												235			245	
gcc	acc	gat	gag	gag	gcc	ctc	gac	tgg	gtc	cag	gac	ctc	atc	tcc	ttc	1124
Ala	Thr	Asp	Glu	Glu	Ala	Leu	Asp	Trp	Val	Gln	Asp	Leu	Ile	Ser	Phe	
												250			260	
ctg	ccc	tcc	aat	cgc	tcc	tac	gcc	ccg	gtg	gag	gag	ttc	gac	gag		1172
Leu	Pro	Ser	Asn	Asn	Arg	Ser	Tyr	Ala	Pro	Val	Glu	Glu	Phe	Asp	Glu	
												265			275	
gag	gac	ggt	ggc	atc	gcc	gag	aac	atc	acc	gcc	gat	gac	ctg	aag	ctg	1220
Glu	Asp	Gly	Gly	Ile	Ala	Glu	Asn	Ile	Thr	Ala	Asp	Asp	Leu	Lys	Leu	
												280			290	
gat	gag	atc	atc	ccg	gat	tcc	gcc	acc	gtg	ccc	tat	gat	gtc	cgc	gac	1268
Asp	Glu	Ile	Ile	Pro	Asp	Ser	Ala	Thr	Val	Pro	Tyr	Asp	Val	Arg	Asp	
												295			310	
gtc	atc	cag	tgc	ctg	acc	gac	gac	ggt	gag	tac	ctg	gag	atc	cag	gcc	1316
Val	Ile	Gln	Cys	Leu	Thr	Asp	Asp	Gly	Glu	Tyr	Leu	Glu	Ile	Gln	Ala	
												315			325	
gac	cga	gcc	gag	aat	gtc	gtc	atc	gcc	ttc	ggc	cgc	atc	gag	ggc	cag	1364
Asp	Arg	Ala	Glu	Asn	Val	Val	Ile	Ala	Phe	Gly	Arg	Ile	Glu	Gly	Gln	
												330			340	
tcc	gtc	ggt	ttc	gtc	gcc	aac	cag	ccg	acc	cag	ttc	gcc	ggc	tgc	ctg	1412
Ser	Val	Gly	Phe	Val	Ala	Asn	Gln	Pro	Thr	Gln	Phe	Ala	Gly	Cys	Leu	
												345			355	
gac	atc	gac	tcc	tcc	gag	aag	gca	gcc	cgc	ttc	gtc	cgc	acc	tgc	gat	1460
Asp	Ile	Asp	Ser	Ser	Glu	Lys	Ala	Ala	Arg	Phe	Val	Arg	Thr	Cys	Asp	
												360			370	
gcc	ttc	aac	atc	ccg	atc	gtc	atg	ctt	gtc	gac	gtc	ccc	ggc	ttc	ctc	1508

Ala	Phe	Asn	Ile	Pro	Ile	Val	Met	Leu	Val	Asp	Val	Pro	Gly	Phe	Leu	
375					380				385					390		
ccc	ggc	ggc	cag	gag	tac	ggc	ggc	atc	ctg	cgt	cgt	ggc	ggc	aaa		1556
Pro	Gly	Ala	Gly	Gln	Glu	Tyr	Gly	Gly	Ile	Leu	Arg	Arg	Gly	Ala	Lys	
									395	400				405		
ctg	ctc	tac	gcc	tac	ggt	gag	gcc	acc	gtc	ccg	aag	atc	acc	gtg	acc	1604
Leu	Leu	Tyr	Ala	Tyr	Gly	Glu	Ala	Thr	Val	Pro	Lys	Ile	Thr	Val	Thr	
								410	415				420			
atg	cgc	aag	gcc	tac	ggc	ggt	gcg	tac	tgt	gtc	atg	gga	tcc	aag	ggt	1652
Met	Arg	Lys	Ala	Tyr	Gly	Gly	Ala	Tyr	Cys	Val	Met	Gly	Ser	Lys	Gly	
								425	430				435			
ctg	ggc	gca	gac	atc	aac	ctg	gcc	tgg	ccg	acc	gcg	cag	atc	gcc	gtc	1700
Leu	Gly	Ala	Asp	Ile	Asn	Leu	Ala	Trp	Pro	Thr	Ala	Gln	Ile	Ala	Val	
						440	445				450					
atg	ggt	gcc	gcc	ggc	ggt	gtc	cag	tcc	atc	tac	cgc	aag	gag	ctc	atg	1748
Met	Gly	Ala	Ala	Gly	Ala	Val	Gln	Phe	Ile	Tyr	Arg	Lys	Glu	Leu	Met	
						455	460			465				470		
gcc	gct	gat	gcc	aag	ggc	ctg	gac	acc	gtc	gcc	ctg	gcc	cag	tcc	tcc	1796
Ala	Ala	Asp	Ala	Lys	Gly	Leu	Asp	Thr	Val	Ala	Leu	Ala	Gln	Ser	Phe	
						475			480					485		
gag	cgt	gag	tac	gag	gac	cac	atg	ctc	aac	ccg	tac	ctg	gcg	gcc	gag	1844
Glu	Arg	Glu	Tyr	Glu	Asp	His	Met	Leu	Asn	Pro	Tyr	Leu	Ala	Ala	Glu	
						490			495					500		
cgt	ggc	ctc	atc	gac	gct	gtg	atc	ctg	ccg	tcc	gag	acc	cgt	ggc	cag	1892
Arg	Gly	Leu	Ile	Asp	Ala	Val	Ile	Leu	Pro	Ser	Glu	Thr	Arg	Gly	Gln	
						505			510					515		
atc	gca	cgc	aac	ctg	cgt	ctg	ctc	aag	cac	aag	aat	gtc	tcc	cgc	cct	1940
Ile	Ala	Arg	Asn	Leu	Arg	Leu	Leu	Lys	His	Lys	Asn	Val	Ser	Arg	Pro	
						520			525					530		
gcc	cgc	aag	cac	ggc	aac	atg	cca	ctg	taagcaccgg	ggaccacccc						1987
Ala	Arg	Lys	His	Gly	Asn	Met	Pro	Leu								
						535			540							
ctacgcccc	acccacggcc	ctttgctggc	aggtgcgggc	gctgtgcgtt	ttccgcgcct											2047
gccgacgccc	ggccccctgc	cctgtatgc	gatctgcgga	tgtatctgc	gcccgccca											2107
actccccctgg	ttgaaccctg	c														2128

<210> 6  
<211> 543  
<212> PRT  
<213> Corynebacterium thermoaminogenes

Met	Thr	Ile	Ser	Ser	Pro	Leu	Ile	Asp	Val	Ala	Asn	Leu	Pro	Asp	Ile	
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Asn	Thr	Thr	Ala	Gly	Lys	Ile	Ala	Asp	Leu	Lys	Ala	Arg	Arg	Ala	Glu	
						20			25					30		
Ala	His	Phe	Pro	Met	Gly	Glu	Lys	Ala	Val	Glu	Lys	Val	His	Ala	Ala	
						35			40					45		
Asn	Arg	Leu	Thr	Ala	Arg	Glu	Arg	Leu	Asp	Tyr	Leu	Leu	Asp	Glu	Gly	
						50			55					60		
Ser	Phe	Ile	Glu	Thr	Asp	Gln	Leu	Ala	Arg	His	Arg	Thr	Thr	Ala	Phe	

65	70	75	80
Gly Leu Gly Asn Lys Arg Pro Ala Thr Asp	Gly Ile Val Thr Gly Trp		
85	90		95
Gly Thr Ile Asp Gly Arg Glu Val Cys	Ile Phe Ser Gln Asp Gly Thr		
100	105		110
Val Phe Gly Gly Ala Leu Gly Glu Val Tyr	Gly Glu Lys Met Ile Lys		
115	120		125
Ile Met Glu Leu Ala Ile Asp Thr Gly Arg	Pro Leu Ile Gly Leu Tyr		
130	135		140
Glu Gly Ala Gly Ala Arg Ile Gln Asp Gly	Ala Val Ser Leu Asp Phe		
145	150		160
Ile Ser Gln Thr Phe Tyr Gln Asn Ile Gln	Ala Ser Gly Val Ile Pro		
165	170		175
Gln Ile Ser Val Ile Met Gly Ala Cys Ala	Gly Gly Asn Ala Tyr Gly		
180	185		190
Pro Ala Leu Thr Asp Phe Val Val Met Val	Asp Lys Thr Ser Lys Met		
195	200		205
Phe Val Thr Gly Pro Asp Val Ile Lys Thr	Val Thr Gly Glu Glu Ile		
210	215		220
Thr Gln Glu Glu Leu Gly Gly Ala Thr Thr	His Met Val Thr Ala Gly		
225	230		240
Asn Ser His Tyr Thr Val Ala Thr Asp Glu	Glu Ala Leu Asp Trp Val		
245	250		255
Gln Asp Leu Ile Ser Phe Leu Pro Ser Asn	Asn Arg Ser Tyr Ala Pro		
260	265		270
Val Glu Glu Phe Asp Glu Glu Asp Gly Gly	Ile Ala Glu Asn Ile Thr		
275	280		285
Ala Asp Asp Leu Lys Leu Asp Glu Ile Ile	Pro Asp Ser Ala Thr Val		
290	295		300
Pro Tyr Asp Val Arg Asp Val Ile Gln Cys	Leu Thr Asp Asp Gly Glu		
305	310		320
Tyr Leu Glu Ile Gln Ala Asp Arg Ala Glu	Asn Val Val Ile Ala Phe		
325	330		335
Gly Arg Ile Glu Gly Gln Ser Val Gly Phe	Val Ala Asn Gln Pro Thr		
340	345		350
Gln Phe Ala Gly Cys Leu Asp Ile Asp Ser	Ser Glu Lys Ala Ala Arg		
355	360		365
Phe Val Arg Thr Cys Asp Ala Phe Asn Ile	Pro Ile Val Met Leu Val		
370	375		380
Asp Val Pro Gly Phe Leu Pro Gly Ala Gly	Gln Glu Tyr Gly Gly Ile		
385	390		400
Leu Arg Arg Gly Ala Lys Leu Leu Tyr Ala	Tyr Gly Glu Ala Thr Val		
405	410		415
Pro Lys Ile Thr Val Thr Met Arg Lys Ala	Tyr Gly Gly Ala Tyr Cys		
420	425		430
Val Met Gly Ser Lys Gly Leu Gly Ala Asp	Ile Asn Leu Ala Trp Pro		
435	440		445
Thr Ala Gln Ile Ala Val Met Gly Ala Ala	Gly Ala Val Gln Phe Ile		
450	455		460
Tyr Arg Lys Glu Leu Met Ala Ala Asp Ala	Lys Gly Leu Asp Thr Val		
465	470		475
			480

Ala	Leu	Ala	Gln	Ser	Phe	Glu	Arg	Glu	Tyr	Glu	Asp	His	Met	Leu	Asn
					485				490					495	
Pro	Tyr	Leu	Ala	Ala	Glu	Arg	Gly	Leu	Ile	Asp	Ala	Val	Ile	Leu	Pro
					500				505					510	
Ser	Glu	Thr	Arg	Gly	Gln	Ile	Ala	Arg	Asn	Leu	Arg	Leu	Leu	Lys	His
					515				520					525	
Lys	Asn	Val	Ser	Arg	Pro	Ala	Arg	Lys	His	Gly	Asn	Met	Pro	Leu	
					530				535					540	

<210> 7

<211> 2076

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (412)..(2022)

<400> 7

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acgggggggaa	ggaggtcaca	taggccatac	gctgcacttt	tgatgaagtg	tgggcagatc	180
gaccggggcaa	atctgggaaa	taaggggcct	ggtgaactag	cattcccctt	agcgaagggt	240
gagcatcgcg	gaccccgcga	tgtcccaacc	ggtcgtaaat	tcatgtgccc	ccacagtccc	300
ctcaccaggg	gatcggAAC	agcccagcct	gattccggcg	tgacggacct	caccgtgaac	360
aagtccccgc	attactcaca	gaactcacac	caggatttag	actaagaaac	c atg act	417
					Met Thr	
					1	

gca	gca	acg	aca	gca	cct	gat	ctg	acc	acc	acc	gcc	ggc	aaa	ctc	gcg	465
Ala	Ala	Thr	Thr	Ala	Pro	Asp	Leu	Thr	Thr	Thr	Ala	Gly	Lys	Leu	Ala	
							5	10			15					
gat	ctc	cgc	gcc	cgc	ctt	tcc	gag	acc	cag	gcc	ccc	atg	ggt	cag	gcc	513
Asp	Leu	Arg	Ala	Arg	Leu	Ser	Glu	Thr	Gln	Ala	Pro	Met	Gly	Gln	Ala	
							20	25			30					
tcc	gtg	gag	aag	gtg	cac	gag	gca	ggg	aag	aag	acc	gca	cgc	gag	cgc	561
Ser	Val	Glu	Lys	Val	His	Glu	Ala	Gly	Lys	Lys	Thr	Ala	Arg	Glu	Arg	
							35	40			45			50		
atc	gag	tac	ctg	ctc	gat	gag	ggc	tcc	tcc	gtt	gag	gtc	gat	gcc	ctc	609
Ile	Glu	Tyr	Leu	Leu	Asp	Glu	Gly	Ser	Phe	Val	Glu	Val	Asp	Ala	Leu	
							55		60			65				
gcc	cgc	cac	cgt	tcc	aag	aac	ttc	ggc	ctg	gac	tcc	aag	cgc	ccg	gtc	657
Ala	Arg	His	Arg	Ser	Lys	Asn	Phe	Gly	Leu	Asp	Ser	Lys	Arg	Pro	Val	
							70		75			80				
acc	gac	ggt	gtg	gtc	acc	ggt	tac	ggc	acc	atc	gac	gga	cgc	aag	gtc	705
Thr	Asp	Gly	Val	Val	Thr	Gly	Tyr	Gly	Thr	Ile	Asp	Gly	Arg	Lys	Val	
							85		90			95				
tgc	gtc	ttc	tcc	cag	gac	ggc	gct	atc	tcc	ggc	ggt	gcc	ctc	ggt	gag	753
Cys	Val	Phe	Ser	Gln	Asp	Gly	Ala	Ile	Phe	Gly	Gly	Ala	Leu	Gly	Glu	
							100		105			110				
gtc	tac	ggc	gag	aag	atc	gtc	aag	atc	atg	gac	ctg	gcc	atc	aag	acc	801
Val	Tyr	Gly	Glu	Lys	Ile	Val	Lys	Ile	Met	Asp	Leu	Ala	Ile	Lys	Thr	

115	120	125	130	
ggt gtc ccc ctc atc ggc atc aac gag ggc ggc gcc ggc cgc atc cag				849
Gly Val Pro Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg Ile Gln				
135	140	145		
gaa ggc gtt gtc tcc ctg ggc ctg tac tcc cag atc ttc tac cgc aac				897
Glu Gly Val Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr Arg Asn				
150	155	160		
acc cag gca tcc ggt gtc atc cca cag atc tcc ctc atc atg ggt gcc				945
Thr Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met Gly Ala				
165	170	175		
tgc gcc ggt ggc cat gtg tac tcc ccc gcc ctg acc gac ttc atc atc				993
Cys Ala Gly Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe Ile Ile				
180	185	190		
atg gtg gac aag acc tcc aag atg ttc atc acc ggc ccc gac gtg atc				1041
Met Val Asp Lys Thr Ser Lys Met Phe Ile Thr Gly Pro Asp Val Ile				
195	200	205	210	
aag acc gtc acc ggc gag gag gtc acc cag gag gaa ctg ggt ggt gcc				1089
Lys Thr Val Thr Gly Glu Glu Val Thr Gln Glu Glu Leu Gly Gly Ala				
215	220	225		
tac acc cac atg gcc cag tcc ggc acc tcg cac tac acc gca gcc gat				1137
Tyr Thr His Met Ala Gln Ser Gly Thr Ser His Tyr Thr Ala Ala Asp				
230	235	240		
gac tcc gat gcc ctc gac tgg gtc cgt gag ctg gtc agc tac ctg ccg				1185
Asp Ser Asp Ala Leu Asp Trp Val Arg Glu Leu Val Ser Tyr Leu Pro				
245	250	255		
tcc aac aac cgt gcg gag acc cca cgc cag gac gcc gac atc atg gtg				1233
Ser Asn Asn Arg Ala Glu Thr Pro Arg Gln Asp Ala Asp Ile Met Val				
260	265	270		
ggc tcc atc aag gag aac atc acc gag acc gac ctc gaa ctc gac acc				1281
Gly Ser Ile Lys Glu Asn Ile Thr Glu Thr Asp Leu Glu Leu Asp Thr				
275	280	285	290	
ctg atc ccg gat tcc ccg aac cag ccg tac gac atg aag gac gtc atc				1329
Leu Ile Pro Asp Ser Pro Asn Gln Pro Tyr Asp Met Lys Asp Val Ile				
295	300	305		
acc cgc atc gtc gat gat gcc gag ttc ttc gag atc cag gag ggt tac				1377
Thr Arg Ile Val Asp Asp Ala Glu Phe Phe Glu Ile Gln Glu Gly Tyr				
310	315	320		
gcc gag aac atc atc tgc ggt ttc gcc cgc gtc gag ggt cgt gcc gtg				1425
Ala Glu Asn Ile Ile Cys Gly Phe Ala Arg Val Glu Gly Arg Ala Val				
325	330	335		
ggt atc gtg gcc aac cag ccg atg cag ttc gcc ggc tgc ctg gac atc				1473
Gly Ile Val Ala Asn Gln Pro Met Gln Phe Ala Gly Cys Leu Asp Ile				
340	345	350		
aag gca tcc gag aag gcc gcc cgc ttc atc cgc acc tgt gac gcc ttc				1521
Lys Ala Ser Glu Lys Ala Ala Arg Phe Ile Arg Thr Cys Asp Ala Phe				
355	360	365	370	
aac atc ccg atc atc gag ctt gtc gac gtc cca ggc ttc ctc ccg ggc				1569
Asn Ile Pro Ile Ile Glu Leu Val Asp Val Pro Gly Phe Leu Pro Gly				
375	380	385		
acc aac cag gag ttc gac ggc atc atc cgt cgc ggc gcg aag ctg ctc				1617
Thr Asn Gln Glu Phe Asp Gly Ile Ile Arg Arg Gly Ala Lys Leu Leu				

390	395	400	
tac	gcc	acc	1665
Tyr	Ala	Glu	
405	410	415	
aag	tcc	gtc	1713
Lys	Ser	Gly	
420	425	430	
gac	ctc	tgg	1761
Ala	Asp	Leu	
435	440	445	
ggt	gcc	ccc	
Ala	Ser	acc	1809
455	460	465	
gca	gct	gct	1857
Ala	Ala	gag	
470	475	480	
gag	tac	acc	1905
Glu	Tyr	Glu	
485	490	495	
gac	gtc	atc	1953
Tyr	Val	Asp	
500	505	510	
ggt	ctg	ccg	2001
Glu	Gly	Leu	
515	520	525	
aag	cac	atc	2052
Lys	His	Gly	
535			
gagaaggctt	tgtccgcagc	tgtc	2076

<210> 8

<211> 537

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 8

Met	Thr	Ala	Ala	Thr	Thr	Ala	Pro	Asp	Leu	Thr	Thr	Ala	Gly	Lys
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Leu	Ala	Asp	Leu	Arg	Ala	Arg	Leu	Ser	Glu	Thr	Gln	Ala	Pro	Met
				20						25				30
Gln	Ala	Ser	Val	Glu	Lys	Val	His	Glu	Ala	Gly	Lys	Lys	Thr	Ala
				35						40				45
Glu	Arg	Ile	Glu	Tyr	Leu	Leu	Asp	Glu	Gly	Ser	Phe	Val	Glu	Val
		50									60			
Ala	Leu	Ala	Arg	His	Arg	Ser	Lys	Asn	Phe	Gly	Leu	Asp	Ser	Lys
											75			80
Pro	Val	Thr	Asp	Gly	Val	Val	Thr	Gly	Tyr	Gly	Thr	Ile	Asp	Gly
											90			95
Lys	Val	Cys	Val	Phe	Ser	Gln	Asp	Gly	Ala	Ile	Phe	Gly	Gly	Ala
											105			110
Gly	Glu	Val	Tyr	Gly	Glu	Lys	Ile	Val	Lys	Ile	Met	Asp	Leu	Ala
														Ile

115	120	125	
Lys Thr Gly Val Pro Leu Ile	Gly Ile Asn Glu Gly Ala Gly Ala Arg		
130	135	140	
Ile Gln Glu Gly Val Val	Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr		
145	150	155	160
Arg Asn Thr Gln Ala Ser Gly Val Ile	Pro Gln Ile Ser Leu Ile Met		
165	170	175	
Gly Ala Cys Ala Gly Gly His Val	Tyr Ser Pro Ala Leu Thr Asp Phe		
180	185	190	
Ile Ile Met Val Asp Lys Thr	Ser Lys Met Phe Ile Thr Gly Pro Asp		
195	200	205	
Val Ile Lys Thr Val Thr Gly	Glu Glu Val Thr Gln Glu Glu Leu Gly		
210	215	220	
Gly Ala Tyr Thr His Met Ala	Gln Ser Gly Thr Ser His Tyr Thr Ala		
225	230	235	240
Ala Asp Asp Ser Asp Ala	Leu Asp Trp Val Arg Glu Leu Val Ser Tyr		
245	250	255	
Leu Pro Ser Asn Asn Arg Ala	Glu Thr Pro Arg Gln Asp Ala Asp Ile		
260	265	270	
Met Val Gly Ser Ile Lys Glu	Asn Ile Thr Glu Thr Asp Leu Glu Leu		
275	280	285	
Asp Thr Leu Ile Pro Asp Ser	Pro Asn Gln Pro Tyr Asp Met Lys Asp		
290	295	300	
Val Ile Thr Arg Ile Val Asp	Asp Ala Glu Phe Phe Glu Ile Gln Glu		
305	310	315	320
Gly Tyr Ala Glu Asn Ile	Ile Cys Gly Phe Ala Arg Val Glu Gly Arg		
325	330	335	
Ala Val Gly Ile Val Ala Asn	Gln Pro Met Gln Phe Ala Gly Cys Leu		
340	345	350	
Asp Ile Lys Ala Ser Glu Lys	Ala Ala Arg Phe Ile Arg Thr Cys Asp		
355	360	365	
Ala Phe Asn Ile Pro Ile	Ile Glu Leu Val Asp Val Pro Gly Phe Leu		
370	375	380	
Pro Gly Thr Asn Gln Glu	Phe Asp Gly Ile Ile Arg Arg Gly Ala Lys		
385	390	395	400
Leu Leu Tyr Ala Tyr Ala	Glu Ala Thr Val Gly Lys Ile Thr Val Ile		
405	410	415	
Thr Arg Lys Ser Tyr Gly	Gly Ala Tyr Cys Val Met Gly Ser Lys Asp		
420	425	430	
Met Gly Ala Asp Leu Val	Phe Ala Trp Pro Thr Ala Gln Ile Ala Val		
435	440	445	
Met Gly Ala Ser Gly Ala	Val Gly Phe Ile Tyr Arg Lys Glu Leu Lys		
450	455	460	
Gln Ala Ala Ala Gly	Glu Asp Val Thr Ala Leu Met Lys Lys Tyr		
465	470	475	480
Glu Gln Glu Tyr Glu	Glu Thr Leu Val Asn Pro Tyr Met Ala Ala Glu		
485	490	495	
Arg Gly Tyr Val Asp Ala Val	Ile Pro Pro Ser Glu Thr Arg Gly Gln		
500	505	510	
Ile Ile Glu Gly Leu Arg	Leu Leu Asp Arg Lys Val Val Asn Val Pro		
515	520	525	

Ala Lys Lys His Gly Asn Ile Pro Leu  
530 535

<210> 9  
<211> 1643  
<212> DNA  
<213> Corynebacterium thermoaminogenes

<220>  
<221> CDS  
<222> (326)..(1363)

<400> 9  
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tcagccaccc gccgatgaga cctgcagcga caacgggtgc ggtgctgacc tggtcagcgt 120  
ctttgagtt catatccatg tcagacagtc taaccactct ctccgacgcg tccgaacatg 180  
ctgggtggc ggacaccatg tccgttcggg cgttgccccg acgggggaaa atcgcaggca 240  
gatgtgtccg atgtggata aaccaccggg ttcgggcgtg tcttcggat caatggcaca 300  
gcattaaccg tgtgggggt ttaat atg gga gcc atg cga att gcc act ctc 352  
Met Gly Ala Met Arg Ile Ala Thr Leu  
1 5  
acg tca ggc ggc gac tgc ccc gga ctc aat gct gtc atc agg gga atc 400  
Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val Ile Arg Gly Ile  
10 15 20 25  
gtc cgt acc gca agt aat gaa ttc ggt tcc acc gtc gtg ggt tat cag 448  
Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val Val Gly Tyr Gln  
30 35 40  
gac ggc tgg gag ggc ctg ctg gcg gac cga cgt gtt cag ctc tat gac 496  
Asp Gly Trp Glu Gly Leu Leu Ala Asp Arg Arg Val Gln Leu Tyr Asp  
45 50 55  
gat gag gac atc gac cgc atc ctg ctc cgc ggt gga aca atc ctg ggc 544  
Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly Thr Ile Leu Gly  
60 65 70  
acc ggt cgt ctc cac ccc gac aag ttc aga gcc gga atc gac cag gtc 592  
Thr Gly Arg Leu His Pro Asp Lys Phe Arg Ala Gly Ile Asp Gln Val  
75 80 85  
aag gcg aat ctc gcc gat gcg gga att gac gca ctc atc ccg atc ggt 640  
Lys Ala Asn Leu Ala Asp Ala Gly Ile Asp Ala Leu Ile Pro Ile Gly  
90 95 100 105  
ggc gag ggc acc ctc aag gga gcg aag tgg ctc gcc gac aac ggc atc 688  
Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ala Asp Asn Gly Ile  
110 115 120  
ccc gtg gtc ggt gtc ccg aaa acc atc gac aat gat gtc aac ggc acg 736  
Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp Val Asn Gly Thr  
125 130 135  
gat ttc acc ttc ggt ttc gat tcc gcg gtc tct gtg gcc acc gac gcc 784  
Asp Phe Thr Phe Gly Phe Asp Ser Ala Val Ser Val Ala Thr Asp Ala  
140 145 150  
atc gac cgg ctg cac acc acg gcg gaa tcc cac aac cgt gtg atg atc 832  
Ile Asp Arg Leu His Thr Thr Ala Glu Ser His Asn Arg Val Met Ile  
155 160 165

gtc gag gtc atg ggc cgc cac gtc ggt tgg atc gca ctg cat gcc ggc 880  
 Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala Leu His Ala Gly  
 170 175 180 185  
 atg gcc ggt gga gcc cac tac acc gtc atc ccc gag gtg ccc ttc gac 928  
 Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu Val Pro Phe Asp  
 190 195 200  
 atc tcg gag atc tgc aag cgt atg gaa cgt cgc ttc cag atg ggg gag 976  
 Ile Ser Glu Ile Cys Lys Arg Met Glu Arg Arg Phe Gln Met Gly Glu  
 205 210 215  
 aag tac ggc atc atc gtc gtc gcg gag ggt gcc ctg ccc aag gag gga 1024  
 Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu Pro Lys Glu Gly  
 220 225 230  
 acc atg gag ctg cgt gag ggg gag gtg gat cag ttc ggt cac aag acc 1072  
 Thr Met Glu Leu Arg Glu Gly Glu Val Asp Gln Phe Gly His Lys Thr  
 235 240 245  
 ttc acc ggc atc ggc cag cag atc gcc gac gag gtg cac agg cgt ctg 1120  
 Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Val His Arg Arg Leu  
 250 255 260 265  
 ggt cat gat gtc cgc acc acg gtc ctg ggc cat atc cag cgt ggt ggc 1168  
 Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile Gln Arg Gly Gly  
 270 275 280  
 acc ccc acc gcc ttc gac cgt gtc ctg gcc acc cgg tac ggt gtc cgc 1216  
 Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg Tyr Gly Val Arg  
 285 290 295  
 gcc gcg cgt gcc tgc cac gag ggt cag ttc aac acc gtg gtc gcg ctc 1264  
 Ala Ala Arg Ala Cys His Glu Gly Gln Phe Asn Thr Val Val Ala Leu  
 300 305 310  
 aag ggg gag cgc atc cgg atg atc tcc ttc gat gag gcc gtg ggc acc 1312  
 Lys Gly Glu Arg Ile Arg Met Ile Ser Phe Asp Glu Ala Val Gly Thr  
 315 320 325  
 ctg aag aag gtg ccg atg gaa cgc tgg gtg acc gcc cag gct atg ttc 1360  
 Leu Lys Lys Val Pro Met Glu Arg Trp Val Thr Ala Gln Ala Met Phe  
 330 335 340 345  
 ggt tagtcaggcc gcattcccg ttccgcgccc gcggggccgg gttttttcat 1413  
 Gly  
 gccccggAAC acatcggtat gaaatcgtga tatgcattac ttgacggggaa agtggggat 1473  
 ccgtcacctc gcgttgtcca actacagccc gcagcgctg cggaaattct tcgagcaatc 1533  
 cggccattcc cccggcccgcc cctgcgcgtt ccaaccgcag tacaatctgc tggcccgccg 1593  
 ggattatgag accggtatcc gcccggcgtt ggacgagttc ggtcccgccg 1643

<210> 10  
 <211> 346  
 <212> PRT  
 <213> Corynebacterium thermoaminogenes

<400> 10  
 Met Gly Ala Met Arg Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro  
 1 5 10 15  
 Gly Leu Asn Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu  
 20 25 30  
 Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu

35	40	45
Ala Asp Arg Arg Val Gln Leu Tyr	Asp Asp Glu Asp	Ile Asp Arg Ile
50 55 60		
Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp		
65 70 75 80		
Lys Phe Arg Ala Gly Ile Asp Gln Val Lys Ala Asn Leu Ala Asp Ala		
85 90 95		
Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly		
100 105 110		
Ala Lys Trp Leu Ala Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys		
115 120 125		
Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp		
130 135 140		
Ser Ala Val Ser Val Ala Thr Asp Ala Ile Asp Arg Leu His Thr Thr		
145 150 155 160		
Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His		
165 170 175		
Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr		
180 185 190		
Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ser Glu Ile Cys Lys Arg		
195 200 205		
Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val		
210 215 220		
Ala Glu Gly Ala Leu Pro Lys Glu Gly Thr Met Glu Leu Arg Glu Gly		
225 230 235 240		
Glu Val Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln		
245 250 255		
Ile Ala Asp Glu Val His Arg Arg Leu Gly His Asp Val Arg Thr Thr		
260 265 270		
Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg		
275 280 285		
Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu		
290 295 300		
Gly Gln Phe Asn Thr Val Val Ala Leu Lys Gly Glu Arg Ile Arg Met		
305 310 315 320		
Ile Ser Phe Asp Glu Ala Val Gly Thr Leu Lys Lys Val Pro Met Glu		
325 330 335		
Arg Trp Val Thr Ala Gln Ala Met Phe Gly		
340 345		

<210> 11

<211> 498

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1)..(498)

<400> 11

tac tac cag cac gat cca ggt ttc ccc ttc gca cca aag cgc acc ggt

48

Tyr	Tyr	Gln	His	Asp	Pro	Gly	Phe	Pro	Phe	Ala	Pro	Lys	Arg	Thr	Gly	
1				5				10						15		
tgg	gct	cac	acc	acc	acg	ccg	ttg	acc	gga	ccg	cag	cga	ttg	cag	tgg	96
Trp	Ala	His	Thr	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gln	Arg	Leu	Gln	Trp	
				20				25					30			
acg	cac	ctg	ccc	gat	gct	ctt	tac	ccg	gat	gta	tcc	tat	gac	ctg	gat	144
Thr	His	Leu	Pro	Asp	Ala	Leu	Tyr	Pro	Asp	Val	Ser	Tyr	Asp	Leu	Asp	
				35				40				45				
gga	tgc	tat	tcc	ggc	gga	gcc	gta	ttt	tct	gac	ggc	acg	ctt	aaa	ctt	192
Gly	Cys	Tyr	Ser	Gly	Gly	Ala	Val	Phe	Ser	Asp	Gly	Thr	Leu	Lys	Leu	
				50				55			60					
ttc	tac	acc	ggc	aac	cga	aaa	att	gac	ggc	aag	cgc	cgc	gcc	acc	caa	240
Phe	Tyr	Thr	Gly	Asn	Arg	Lys	Ile	Asp	Gly	Lys	Arg	Arg	Ala	Thr	Gln	
				65				70			75			80		
aac	ctc	gtc	gaa	gtc	gag	gac	cca	act	ggg	ctg	atg	ggc	ggc	att	cat	288
Asn	Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	Leu	Met	Gly	Gly	Ile	His	
				85					90			95				
cgc	cgc	tcg	cct	aaa	aat	ccg	ctt	atc	gac	gga	ccc	gcc	agc	ggt	ttt	336
Arg	Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	Ala	Ser	Gly	Phe	
				100				105			110					
acg	ccc	cac	tac	cgc	gat	ccc	atg	atc	agc	cct	gat	ggg	gat	ggt	tgg	384
Thr	Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	Gly	Asp	Gly	Trp	
				115				120			125					
aag	atg	gtt	ctt	ggg	gct	cag	cgc	gaa	aac	ctc	acc	ggt	gca	gcg	gtt	432
Lys	Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	Gly	Ala	Ala	Val	
				130				135			140					
cta	tac	cgc	tcg	gca	gat	ctt	gaa	aac	tgg	gaa	ttc	tcc	ggt	gaa	atc	480
Leu	Tyr	Arg	Ser	Ala	Asp	Leu	Glu	Asn	Trp	Glu	Phe	Ser	Gly	Glu	Ile	
				145				150			155			160		
acc	ttt	gac	ctc	agc	gac											498
Thr	Phe	Asp	Leu	Ser	Asp											
				165												

<210> 12  
<211> 166  
<212> PRT  
<213> Corynebacterium thermoaminogenes

Tyr	Tyr	Gln	His	Asp	Pro	Gly	Phe	Pro	Phe	Ala	Pro	Lys	Arg	Thr	Gly	
1				5				10					15			
Trp	Ala	His	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gln	Arg	Leu	Gln	Trp		
				20				25				30				
Thr	His	Leu	Pro	Asp	Ala	Leu	Tyr	Pro	Asp	Val	Ser	Tyr	Asp	Leu	Asp	
				35				40			45					
Gly	Cys	Tyr	Ser	Gly	Gly	Ala	Val	Phe	Ser	Asp	Gly	Thr	Leu	Lys	Leu	
				50				55			60					
Phe	Tyr	Thr	Gly	Asn	Arg	Lys	Ile	Asp	Gly	Lys	Arg	Arg	Ala	Thr	Gln	
				65				70			75			80		
Asn	Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	Leu	Met	Gly	Gly	Ile	His	
					85				90			95				

Arg	Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	Ala	Ser	Gly	Phe
100								105						110	
Thr	Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	Gly	Asp	Gly	Trp
115								120						125	
Lys	Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	Gly	Ala	Ala	Val
130								135						140	
Leu	Tyr	Arg	Ser	Ala	Asp	Leu	Glu	Asn	Trp	Glu	Phe	Ser	Gly	Glu	Ile
145								150						155	
Thr	Phe	Asp	Leu	Ser	Asp										
			165												

<210> 13

<211> 479

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1)..(477)

<400> 13

tac	tac	cag	cac	gat	cca	ggt	ttc	ccc	ttc	gca	cca	aag	cgc	acc	ggc	48
Tyr	Tyr	Gln	His	Asp	Pro	Gly	Phe	Pro	Phe	Ala	Pro	Lys	Arg	Thr	Gly	
1		5							10					15		
tgg	gct	cac	acc	acc	acg	ccg	ttg	acc	gga	ccg	cag	cga	ttg	cag	tgg	96
Trp	Ala	His	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gln	Arg	Leu	Gln	Trp		
									25					30		
acg	cac	ctg	ccc	gac	gct	ctt	tac	ccg	gat	gca	tcc	tat	gac	ctg	gat	144
Thr	His	Leu	Pro	Asp	Ala	Leu	Tyr	Pro	Asp	Ala	Ser	Tyr	Asp	Leu	Asp	
									40					45		
gga	tgc	tat	tcc	ggt	gga	gcc	gta	ttt	act	gac	ggc	aca	ctt	aaa	ctt	192
Gly	Cys	Tyr	Ser	Gly	Gly	Ala	Val	Phe	Thr	Asp	Gly	Thr	Leu	Lys	Leu	
									55					60		
ttc	tac	acc	ggc	aac	cta	aaa	att	gac	ggc	aag	cgc	cgc	gcc	acc	caa	240
Phe	Tyr	Thr	Gly	Asn	Leu	Lys	Ile	Asp	Gly	Lys	Arg	Arg	Ala	Thr	Gln	
									70					75		
aac	ctc	gtc	gaa	gtc	gag	gac	cca	act	ggg	ctg	atg	ggc	ggc	att	cat	288
Asn	Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	Leu	Met	Gly	Gly	Ile	His	
									85					90		
cgc	cgt	tcg	cct	aaa	aat	ccg	ctt	atc	gac	gga	ccc	gcc	agc	ggt	ttc	336
Arg	Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	Ala	Ser	Gly	Phe	
									100					105		
aca	ccc	cat	tac	cgc	gat	ccc	atg	atc	agc	cct	gat	ggt	gat	ggt	tgg	384
Thr	Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	Gly	Asp	Gly	Trp	
									115					120		
aaa	atg	gtt	ctt	ggg	gcc	caa	cgc	gaa	aac	ctc	acc	ggt	gca	gcg	gtt	432
Lys	Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	Gly	Ala	Ala	Val	
									130					135		
cta	tac	cgc	tcg	aca	gat	ctt	gaa	aac	tgg	gaa	tcc	tcc	ggt	gaa	at	479
Leu	Tyr	Arg	Ser	Thr	Asp	Leu	Glu	Asn	Trp	Glu	Phe	Ser	Gly	Glu		
									145					150		
														155		

<210> 14  
<211> 159  
<212> PRT  
<213> Corynebacterium thermoaminogenes

<400> 14

Tyr	Tyr	Gln	His	Asp	Pro	Gly	Phe	Pro	Phe	Ala	Pro	Lys	Arg	Thr	Gly
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Trp	Ala	His	Thr	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gln	Arg	Leu	Gln	Trp
				20				25						30	
Thr	His	Leu	Pro	Asp	Ala	Leu	Tyr	Pro	Asp	Ala	Ser	Tyr	Asp	Leu	Asp
				35				40					45		
Gly	Cys	Tyr	Ser	Gly	Gly	Ala	Val	Phe	Thr	Asp	Gly	Thr	Leu	Lys	Leu
					50			55				60			
Phe	Tyr	Thr	Gly	Asn	Leu	Lys	Ile	Asp	Gly	Lys	Arg	Arg	Ala	Thr	Gln
					65		70			75			80		
Asn	Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	Leu	Met	Gly	Gly	Ile	His
					85				90				95		
Arg	Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	Ala	Ser	Gly	Phe
					100			105					110		
Thr	Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	Gly	Asp	Gly	Trp
					115			120				125			
Lys	Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	Gly	Ala	Ala	Val
					130			135				140			
Leu	Tyr	Arg	Ser	Thr	Asp	Leu	Glu	Asn	Trp	Glu	Phe	Ser	Gly	Glu	
					145					155					

<210> 15  
<211> 490  
<212> DNA  
<213> Corynebacterium thermoaminogenes

<400> 15

attttaatgg	atatttatcta	tattttatca	atattatcct	tatgcacctg	aatggggacc	60
aatgcattgg	ggacacgcac	gtagtaaaga	tttagttcat	tggaaacat	taccgattgc	120
tttagaacct	ggagatgaag	aagaaaaatg	gttgtttctc	tggtagatgtt	atagtcaaag	180
atgataagtt	gtatttattt	tatacaggtc	accattatta	taatgacgat	gatcccgatc	240
atttttggca	aaatcaaaat	atggcttata	gtgaagatgg	cattcatttt	caaaaatata	300
aacaaaatgc	aatcattcct	accccacctg	aagataatac	acatcaacttc	agagatccaa	360
aggtatggaa	acatccatgg	cttattatta	catgatagta	ggtagtcaaa	atgatagaga	420
ataggacgt	attatcttat	atcggttctga	ggatttata	agggaaattc	tggtcctgag	480
						490
atcaatccaa						

<210> 16  
<211> 4254  
<212> DNA  
<213> Corynebacterium thermoaminogenes

<220>  
<221> CDS

<222> (637)..(1362)

<220>

<221> CDS

<222> (1434)..(2315)

<220>

<221> CDS

<222> (2432)..(3115)

<220>

<221> CDS

<222> (3235)..(4065)

<400> 16

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cgcagggttt gaagacgatg agatcagggg tgtcaccctc ccccgccgcgt gtgttaaccgg 120  
cctcctcgag cagaccggag agacgctcgg aatcgtggac gttcatctgg cagccgaagg 180  
tacgcacccctc ataggtgcgg gcagtggtgc cctccgggtt ccccccgcgc gggagggtgt 240  
cggcgggggtg gtccgggtgg gatggatggg tggatctg gtgggtatca atctgctgcg 300  
tcacgggagg taattgtatc ggccgcgggc accctgacat aaacgtccga tccagagggaa 360  
cgcaaccccg tggagtgtcg cagccatgca ggttgggcaa caccgtaacg gaacctagca 420  
gagtggtagg attgacttca cattcttac ctattgagct attgataaaa tccgggcgga 480  
aatggaaatc acccccacaa atcacccaa ctgacctgtg gaaaggcgaa gaaatccagg 540  
gaaattcatt tcaaaatgga ctcaatcaca ggatttaccc cacatgaccc aacattcctt 600  
tatgctatcc ccatgacgca gaccacaaat caccgg atg atc aag atg acg ggg 654  
Met Ile Lys Met Thr Gly  
1 5

gtg cag aag ttc ttc gat gac ttc cag gcc ctg acc gat atc aat ctt 702  
Val Gln Lys Phe Phe Asp Asp Phe Gln Ala Leu Thr Asp Ile Asn Leu  
10 15 20

gag gtc ccc gcg gga cag gtc gtt gtt gtt ctc ggc ccg tcc ggt tcc 750  
Glu Val Pro Ala Gly Gln Val Val Val Leu Gly Pro Ser Gly Ser  
25 30 35

gga aag tcg acg ctg tgc cgc acc atc aac cgc ctc gaa acc atc gag 798  
Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn Arg Leu Glu Thr Ile Glu  
40 45 50

gag gga acc atc gag atc gat gga aaa ctg ctt ccg gag gag ggc aag 846  
Glu Gly Thr Ile Glu Ile Asp Gly Lys Leu Leu Pro Glu Glu Gly Lys  
55 60 65 70

gac ctg gcc aag atc cgt gcc gac gtg ggc atg gtg ttc cag tct ttc 894  
Asp Leu Ala Lys Ile Arg Ala Asp Val Gly Met Val Phe Gln Ser Phe  
75 80 85

aac ctc ttc ccc cac ctc acc atc aag gac aat gtc acc ctc ggc ccg 942  
Asn Leu Phe Pro His Leu Thr Ile Lys Asp Asn Val Thr Leu Gly Pro  
90 95 100

atg aag gtc cgg aag atg aag aag tcc gag ggc aat gag gtg gcc atg 990  
Met Lys Val Arg Lys Met Lys Lys Ser Glu Ala Asn Glu Val Ala Met  
105 110 115

aag ctg ttg gaa cgc gtc ggc atc gcc aac cag gcc gag aaa tac ccg 1038  
Lys Leu Leu Glu Arg Val Gly Ile Ala Asn Gln Ala Glu Lys Tyr Pro

120	125	130	
gca cag ctc tcg ggc ggg	cag cag cag cgc gtg	gcc atc gcc cgc gca	1086
Ala Gln Leu Ser Gly Gly	Gln Gln Gln Arg Val	Ala Ile Ala Arg Ala	
135	140	145	150
ctg gcg atg aac ccc aag	atc atg ctt ttc gac	gaa cca acc tcc gcc	1134
Leu Ala Met Asn Pro Lys	Ile Met Leu Phe Asp	Glu Pro Thr Ser Ala	
155	160	165	
ctc gac ccc gag atg gtc	aac gag gtt ctg gac	gtc atg gcg agt ctg	1182
Leu Asp Pro Glu Met Val	Asn Glu Val Leu Asp	Val Met Ala Ser Leu	
170	175	180	
gcc aag gaa ggc atg acc	atg gtg tgt gtc acc	cac gag atg ggt ttc	1230
Ala Lys Glu Gly Met Thr	Met Val Cys Val Thr	His Glu Met Gly Phe	
185	190	195	
gca cgc agg gcc gca gac	cgt gtg ctg ttc atg	tct gac ggc gcc atc	1278
Ala Arg Arg Ala Ala Asp	Arg Val Leu Phe Met	Ser Asp Gly Ala Ile	
200	205	210	
gtc gag gac tcc gac ccg	gag acc ttc ttc acc	aat cca caa acc gac	1326
Val Glu Asp Ser Asp Pro	Glu Thr Phe Phe Thr	Asn Pro Gln Thr Asp	
215	220	225	230
cg <sup>g</sup> g <sup>c</sup> a <sup>a</sup> g <sup>a</sup> g <sup>t</sup> t <sup>t</sup> c <sup>t</sup> g <sup>t</sup> g <sup>g</sup> c <sup>a</sup> a <sup>a</sup> g <sup>t</sup> c <sup>t</sup> c <sup>t</sup> g <sup>c</sup> c <sup>a</sup> c <sup>t</sup> t <sup>g</sup> a <sup>c</sup> c <sup>t</sup> t <sup>cc</sup> c <sup>cc</sup> c <sup>cc</sup>			1372
Arg Ala Lys Asp Phe Leu	Gly Lys Ile Leu Ala	His	
235	240		
tcactctgtg tccaaactccc	ccgctggcca aaatcagcga	ccatgaccaa caggagcatc	1432
a atg tcg cac aaa cgc atg ttc acc cgt	ctc gcc gca gcc acc	acc agc gca	1481
Met Ser His Lys Arg Met	Phe Thr Arg Leu Ala	Ala Ala Thr Ser Ala	
245	250	255	
gct gtt ctc gcc ggc atc acc	ctc acc gcc tgt ggt	gat tcc gag ggt	1529
Ala Val Leu Ala Gly Ile	Thr Leu Thr Ala Cys	Gly Asp Ser Glu Gly	
260	265	270	
ggt gac ggt ctg ctc gcc	gcc atc gaa aat ggc	aat gtc acc atc ggc	1577
Gly Asp Gly Leu Leu Ala	Ala Ile Glu Asn Gly	Asn Val Thr Ile Gly	
275	280	285	290
acc aag tac gat cag ccg	ggt ctg gga ctg cgt	aat ccg gac aat tcc	1625
Thr Lys Tyr Asp Gln Pro	Gly Leu Gly Leu Arg	Asn Pro Asp Asn Ser	
295	300	305	
atg agc gga ctg gat gtc	gac gtc gcg cag tac	gtg gtc aac tcc atc	1673
Met Ser Gly Leu Asp Val	Asp Val Ala Gln Tyr	Val Val Asn Ser Ile	
310	315	320	
gcc gat gac aac ggt tgg	gat cac ccc acc gtg	gaa tgg cgc gag acc	1721
Ala Asp Asp Asn Gly Trp	Asp His Pro Thr Val	Glu Trp Arg Glu Thr	
325	330	335	
ccc tcc gcc cag cgc gag	acc ctc atc cag aac	ggt gag gtg gat atg	1769
Pro Ser Ala Gln Arg Glu	Thr Leu Ile Gln Asn	Gly Glu Val Asp Met	
340	345	350	
atc gcc gca acc tac tcc	atc aac ccc gga cgc	tcc gaa tcg gtg aac	1817
Ile Ala Ala Thr Tyr Ser	Ile Asn Pro Gly Arg	Ser Glu Ser Val Asn	
355	360	365	370
tcc ggt gga cca tac ctc	ctc acc cac cag gcc	ctc ctg gtc cgc gag	1865
Phe Gly Gly Pro Tyr Leu	Leu Thr His Gln Ala	Leu Leu Val Arg Glu	
375	380	385	
gac gat gac cgc atc cag	acc ctc gag gac ctc	gat gac ggc ctg atc	1913

Asp	Asp	Asp	Arg	Ile	Gln	Thr	Leu	Glu	Asp	Leu	Asp	Asp	Gly	Leu	Ile	
				390				395						400		
ctg	tgt	tcc	gtt	acc	gga	tcc	acc	ccc	gcc	cag	aag	gtc	aag	gat	gtc	1961
Leu	Cys	Ser	Val	Thr	Gly	Ser	Thr	Pro	Ala	Gln	Lys	Val	Lys	Asp	Val	
				405				410					415			
ctc	ccc	ggc	gtc	cag	ctg	cag	gaa	tac	gac	acc	tac	tcc	tcc	tgt	gtg	2009
Leu	Pro	Gly	Val	Gln	Leu	Gln	Glu	Tyr	Asp	Thr	Tyr	Ser	Ser	Cys	Val	
				420				425				430				
gag	gca	ctg	agc	cag	ggc	aac	gtc	gat	gca	atg	acc	acc	gac	gcc	acc	2057
Glu	Ala	Leu	Ser	Gln	Gly	Asn	Val	Asp	Ala	Met	Thr	Thr	Asp	Ala	Thr	
				435				440			445			450		
atc	ctc	tcc	ggc	tac	gcg	cag	cag	cgc	gaa	ggt	gaa	ttc	cgc	gtc	gtg	2105
Ile	Leu	Phe	Gly	Tyr	Ala	Gln	Gln	Arg	Glu	Gly	Glu	Phe	Arg	Val	Val	
				455				460					465			
gag	atg	gaa	cag	gac	ggc	gag	ccg	tcc	acc	aat	gag	tac	tac	ggc	atc	2153
Glu	Met	Glu	Gln	Asp	Gly	Glu	Pro	Phe	Thr	Asn	Glu	Tyr	Tyr	Gly	Ile	
				470				475					480			
ggt	atc	acc	aag	gat	gac	acc	gaa	gcc	acc	gat	gcg	atc	aac	gca	gcg	2201
Gly	Ile	Thr	Lys	Asp	Asp	Thr	Glu	Ala	Thr	Asp	Ala	Ile	Asn	Ala	Ala	
				485				490					495			
ttg	gag	cgt	atg	tac	gcc	gac	ggt	tcc	tcc	cag	cgt	ttc	ctc	acc	gag	2249
Leu	Glu	Arg	Met	Tyr	Ala	Asp	Gly	Ser	Phe	Gln	Arg	Phe	Leu	Thr	Glu	
				500				505					510			
aac	ctc	ggc	gag	gat	tcc	cag	gtt	gtc	cag	gag	ggc	acc	ccg	ggt	gac	2297
Asn	Leu	Gly	Glu	Asp	Ser	Gln	Val	Val	Gln	Glu	Gly	Thr	Pro	Gly	Asp	
				515				520			525			530		
ctc	tcc	ttc	ctg	gac	gag	tgac	ctgacg	ggg	ccg	aaacg	ccc	gat	gagc			2345
Leu	Ser	Phe	Leu	Asp	Glu											
				535												
atgcgtggcc	cccgcatccc	gggggtgccac	gcatcatcac	tttc	accact	gatccc	ctac									2405
cgttccttac	cgaggagaaa	ttcccc	atg	agt	aca	tta	tgg	gcg	gat	ctg	ggt					2458
Met	Ser	Thr	Leu	Trp	Ala	Asp	Leu	Gly								
540															545	
ccg	tca	ctc	cta	ccc	gca	ttc	tgg	gtg	aca	atc	caa	ctc	acc	gtc	tat	2506
Pro	Ser	Leu	Leu	Pro	Ala	Phe	Trp	Val	Thr	Ile	Gln	Leu	Thr	Val	Tyr	
				550				555						560		
tcc	gcc	atc	gga	tcc	atg	atc	ctc	ggt	acc	atc	ctc	acc	gcc	atg	agg	2554
Ser	Ala	Ile	Gly	Ser	Met	Ile	Leu	Gly	Thr	Ile	Leu	Thr	Ala	Met	Arg	
				565				570					575			
gtg	tcc	ccg	gtg	aag	atc	ctg	cgc	agc	ata	tcc	acc	gcc	tac	atc	aac	2602
Val	Ser	Pro	Val	Lys	Ile	Leu	Arg	Ser	Ile	Ser	Thr	Ala	Tyr	Ile	Asn	
				580				585					590			
acg	gtc	cgt	aac	acc	cca	ctg	acc	ctg	gtg	atc	ctg	ttc	tgt	tcc	ttc	2650
Thr	Val	Arg	Asn	Thr	Pro	Leu	Thr	Leu	Val	Ile	Leu	Phe	Cys	Ser	Phe	
				595				600					605			
ggc	ctg	tat	cag	aat	ctc	ggt	ctc	acc	ctc	gcc	ggt	cgc	gac	agt	tcc	2698
Gly	Leu	Tyr	Gln	Asn	Leu	Gly	Leu	Thr	Leu	Ala	Gly	Arg	Asp	Ser	Ser	
				610				615			620			625		
acc	ttt	ctg	gcc	gat	aac	aac	ttc	cgg	ctc	gcg	gtg	ctc	gga	ttc	atc	2746
Thr	Phe	Leu	Ala	Asp	Asn	Asn	Phe	Arg	Leu	Ala	Val	Leu	Gly	Phe	Ile	
				630				635					640			

ctg tac acc tcc gcc ttc gtt gcg gaa tca ctc cggttca ggc atc aac	2794
Leu Tyr Thr Ser Ala Phe Val Ala Glu Ser Leu Arg Ser Gly Ile Asn	
645 650 655	
acc gtg cac ttc ggg cag gcg gag gcc cggttca ggc ctc ggt	2842
Thr Val His Phe Gly Gln Ala Glu Ala Ala Arg Ser Leu Gly Leu Gly	
660 665 670	
ttc agt gac atc ttc cggttca atc atc ttc ccc cag gcg gtgtgttca	2890
Phe Ser Asp Ile Phe Arg Ser Ile Ile Phe Pro Gln Ala Val Arg Ala	
675 680 685	
gcc atc atc ccgttca aac acc ctc atc gcc ctgttca acc aag aac acc	2938
Ala Ile Ile Pro Leu Gly Asn Thr Leu Ile Ala Leu Thr Lys Asn Thr	
690 695 700 705	
acg atc gcg tcc gtgttca atc ggc gtc ggt gag gcc tcgttca ctgttca atg aag	2986
Thr Ile Ala Ser Val Ile Gly Val Gly Glu Ala Ser Leu Leu Met Lys	
710 715 720	
tcc acg att gaa aat cat gcc aac atgttca ctc ttc gtc gtgttca gcc atc	3034
Ser Thr Ile Glu Asn His Ala Asn Met Leu Phe Val Val Phe Ala Ile	
725 730 735	
ttc gcc gtc ggc ttc atgttca atc ctc acc ctc ccc atg ggc ctgttca ggg ctt	3082
Phe Ala Val Gly Phe Met Ile Leu Thr Leu Pro Met Gly Leu Gly Leu	
740 745 750	
gga aaa ctc gct gag aaa atg gcg gtgttca aag aaa taatgtccttc ctccgtacgc	3135
Gly Lys Leu Ala Glu Lys Met Ala Val Lys Lys	
755 760	
gcaacagtcc tctacgacgc ccccgcccccc cggggacgca ggtccaaacac catcatcacc	3195
atcgccacca ccctgggtggc agtggccgtc ctgttctgg gtgttca ggc agt gtt ctc	3249
Val Gly Ser Val Leu	
765	
cag gaa aac ggc cag ttg gac ggc gac aaa tgg acc ccgttca ctc gat	3297
Gln Glu Asn Gly Gln Leu Asp Gly Asp Lys Trp Thr Pro Phe Leu Asp	
770 775 780 785	
ccc cag acc tgg acc acc tat ctt ctg ccc ggc ctgttca tgg gga acc ctg	3345
Pro Gln Thr Trp Thr Tyr Leu Leu Pro Gly Leu Trp Gly Thr Leu	
790 795 800	
aag gca gcg gtgttca atc ctt ctc gcg ctgttca atc atg ggc acc ctg	3393
Lys Ala Ala Val Ala Ser Ile Leu Leu Ala Leu Ile Met Gly Thr Leu	
805 810 815	
ctc ggg ctc gga cgc atc tcc gaa atc cggttca ctc ctg cgc tgg ttc tgc	3441
Leu Gly Leu Gly Arg Ile Ser Glu Ile Arg Leu Leu Arg Trp Phe Cys	
820 825 830	
ggg atc atc atc gag acc ttc cgt ggc atc ccgttca gtc atc ctc atg	3489
Gly Ile Ile Ile Glu Thr Phe Arg Ala Ile Pro Val Leu Ile Leu Met	
835 840 845	
atc ttc gcc tat cag ttg ttc gcc cgt tac cag ctc gtt cca tca cgc	3537
Ile Phe Ala Tyr Gln Leu Phe Ala Arg Tyr Gln Leu Val Pro Ser Arg	
850 855 860 865	
cag ctg gcc ttc gcc gcg gtgttca gtc ttc ggt ctc acc atg tac aac ggc	3585
Gln Leu Ala Phe Ala Ala Val Val Phe Gly Leu Thr Met Tyr Asn Gly	
870 875 880	
tcc gtc atc gcc gag atc ctt aga tcgttca ggt atc gcc tcc ctg ccgttca aag	3633
Ser Val Ile Ala Glu Ile Leu Arg Ser Gly Ile Ala Ser Leu Pro Lys	

885	890	895	
gga cag cgt gag gcg gcg atc gcc ctg ggc atg tca acc cgc cag acc			3681
Gly Gln Arg Glu Ala Ala Ile Ala Leu Gly Met Ser Thr Arg Gln Thr			
900	905	910	
acc tgg tcg atc ctg ctc ccc cag gcg gtg gca gcg atg ctg ccc gcc			3729
Thr Trp Ser Ile Leu Leu Pro Gln Ala Val Ala Ala Met Leu Pro Ala			
915	920	925	
ctg atc gcg cag atg gtc atc gcg ctg aag gac tcc gcc ctc ggt tac			3777
Leu Ile Ala Gln Met Val Ile Ala Leu Lys Asp Ser Ala Leu Gly Tyr			
930	935	940	945
cag atc ggt tat atc gag gtg gta cgc tcc ggt atc cag tcc gca tcc			3825
Gln Ile Gly Tyr Ile Glu Val Val Arg Ser Gly Ile Gln Ser Ala Ser			
950	955	960	
gtc aac cgg aac tac ctg gct gcc ctc gcg gtg gtc gcg gtc atc atg			3873
Val Asn Arg Asn Tyr Leu Ala Ala Leu Ala Val Val Ala Val Ile Met			
965	970	975	
atc ctg atc aac ttc gca ctg acc gca ctg gca gag cgt atc cag cgt			3921
Ile Leu Ile Asn Phe Ala Leu Thr Ala Leu Ala Glu Arg Ile Gln Arg			
980	985	990	
cag ctg cgt gcc gga cgt gcc cgc agg aac att gtg gca aag gtg ccc			3969
Gln Leu Arg Ala Gly Arg Ala Arg Arg Asn Ile Val Ala Lys Val Pro			
995	1000	1005	
gag gaa ccc gat cag ggc ctg gat acc aag gac aat gtg aac gtg gat			4017
Glu Glu Pro Asp Gln Gly Leu Asp Thr Lys Asp Asn Val Asn Val Asp			
1010	1015	1020	1025
tgg cac gat ccc gat tac aag gaa gtc aaa cac ccg gga ccg tca ttc			4065
Trp His Asp Pro Asp Tyr Lys Glu Val Lys His Pro Gly Pro Ser Phe			
1030	1035	1040	
tgacaggtcc ctggatcccc gctgcgtca ggaggcggtt gcaacaatga agtccggctg			4125
cccatatgtc tggggcagcc ggactttgtt gcagatcaat gctgactgag gtcctcgatg			4185
cgctcatcga gagcctcccg ggccaggtcc atcgacatac ccgcggggaa tccacgacgg			4245
gcaagtgtct			4254

<210> 17  
 <211> 242  
 <212> PRT  
 <213> Corynebacterium thermoaminogenes

<400> 17			
Met Ile Lys Met Thr Gly Val Gln Lys Phe Phe Asp Asp Phe Gln Ala			
1	5	10	15
Leu Thr Asp Ile Asn Leu Glu Val Pro Ala Gly Gln Val Val Val			
20	25	30	
Leu Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn			
35	40	45	
Arg Leu Glu Thr Ile Glu Glu Gly Thr Ile Glu Ile Asp Gly Lys Leu			
50	55	60	
Leu Pro Glu Glu Gly Lys Asp Leu Ala Lys Ile Arg Ala Asp Val Gly			
65	70	75	80
Met Val Phe Gln Ser Phe Asn Leu Phe Pro His Leu Thr Ile Lys Asp			
85	90	95	

Asn	Val	Thr	Leu	Gly	Pro	Met	Lys	Val	Arg	Lys	Met	Lys	Lys	Ser	Glu
			100					105							110
Ala	Asn	Glu	Val	Ala	Met	Lys	Leu	Leu	Glu	Arg	Val	Gly	Ile	Ala	Asn
			115					120							125
Gln	Ala	Glu	Lys	Tyr	Pro	Ala	Gln	Leu	Ser	Gly	Gly	Gln	Gln	Gln	Arg
			130					135							140
Val	Ala	Ile	Ala	Arg	Ala	Leu	Ala	Met	Asn	Pro	Lys	Ile	Met	Leu	Phe
			145					150							160
Asp	Glu	Pro	Thr	Ser	Ala	Leu	Asp	Pro	Glu	Met	Val	Asn	Glu	Val	Leu
									165						175
Asp	Val	Met	Ala	Ser	Leu	Ala	Lys	Glu	Gly	Met	Thr	Met	Val	Cys	Val
								180							190
Thr	His	Glu	Met	Gly	Phe	Ala	Arg	Arg	Ala	Ala	Asp	Arg	Val	Leu	Phe
								195							205
Met	Ser	Asp	Gly	Ala	Ile	Val	Glu	Asp	Ser	Asp	Pro	Glu	Thr	Phe	Phe
								210							220
Thr	Asn	Pro	Gln	Thr	Asp	Arg	Ala	Lys	Asp	Phe	Leu	Gly	Lys	Ile	Leu
								225							240
Ala	His														

<210> 18

<211> 294

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 18

Met	Ser	His	Lys	Arg	Met	Phe	Thr	Arg	Leu	Ala	Ala	Ala	Thr	Ser	Ala
					1	5			10						15
Ala	Val	Leu	Ala	Gly	Ile	Thr	Leu	Thr	Ala	Cys	Gly	Asp	Ser	Glu	Gly
						20			25						30
Gly	Asp	Gly	Leu	Leu	Ala	Ala	Ile	Glu	Asn	Gly	Asn	Val	Thr	Ile	Gly
							35		40						45
Thr	Lys	Tyr	Asp	Gln	Pro	Gly	Leu	Gly	Leu	Arg	Asn	Pro	Asp	Asn	Ser
							50		55						60
Met	Ser	Gly	Leu	Asp	Val	Asp	Val	Ala	Gln	Tyr	Val	Val	Asn	Ser	Ile
							65		70			75			80
Ala	Asp	Asp	Asn	Gly	Trp	Asp	His	Pro	Thr	Val	Glu	Trp	Arg	Glu	Thr
								85		90					95
Pro	Ser	Ala	Gln	Arg	Glu	Thr	Leu	Ile	Gln	Asn	Gly	Glu	Val	Asp	Met
							100		105						110
Ile	Ala	Ala	Thr	Tyr	Ser	Ile	Asn	Pro	Gly	Arg	Ser	Glu	Ser	Val	Asn
							115		120						125
Phe	Gly	Gly	Pro	Tyr	Leu	Leu	Thr	His	Gln	Ala	Leu	Leu	Val	Arg	Glu
							130		135						140
Asp	Asp	Asp	Arg	Ile	Gln	Thr	Leu	Glu	Asp	Leu	Asp	Asp	Gly	Leu	Ile
							145		150			155			160
Leu	Cys	Ser	Val	Thr	Gly	Ser	Thr	Pro	Ala	Gln	Lys	Val	Lys	Asp	Val
								165		170					175
Leu	Pro	Gly	Val	Gln	Leu	Gln	Glu	Tyr	Asp	Thr	Tyr	Ser	Ser	Cys	Val
							180		185						190
Glu	Ala	Leu	Ser	Gln	Gly	Asn	Val	Asp	Ala	Met	Thr	Thr	Asp	Ala	Thr

195	200	205	
Ile Leu Phe Gly Tyr Ala Gln	Gln Arg Glu Gly Glu	Phe Arg Val Val	
210	215	220	
Glu Met Glu Gln Asp Gly	Glu Pro Phe Thr Asn	Glu Tyr Tyr Gly Ile	
225	230	235	240
Gly Ile Thr Lys Asp Asp	Thr Glu Ala Thr Asp	Ala Ile Asn Ala Ala	
245	250	255	
Leu Glu Arg Met Tyr Ala Asp	Gly Ser Phe Gln Arg	Phe Leu Thr Glu	
260	265	270	
Asn Leu Gly Glu Asp Ser	Gln Val Val Gln Glu	Gly Thr Pro Gly Asp	
275	280	285	
Leu Ser Phe Leu Asp Glu			
290			

<210> 19

<211> 228

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 19

Met Ser Thr Leu Trp Ala Asp	Leu Gly Pro Ser	Leu Leu Pro Ala Phe	
1	5	10	15
Trp Val Thr Ile Gln	Leu Thr Val Tyr	Ser Ala Ile Gly Ser	Met Ile
20	25	30	
Leu Gly Thr Ile Leu Thr Ala	Met Arg Val Ser	Pro Val Lys Ile Leu	
35	40	45	
Arg Ser Ile Ser Thr Ala	Tyr Ile Asn Thr Val	Arg Asn Thr Pro Leu	
50	55	60	
Thr Leu Val Ile Leu Phe	Cys Ser Phe Gly	Leu Tyr Gln Asn Leu	Gly
65	70	75	80
Leu Thr Leu Ala Gly Arg	Asp Ser Ser Thr	Phe Leu Ala Asp Asn	Asn
85	90	95	
Phe Arg Leu Ala Val	Leu Gly Phe Ile	Leu Tyr Thr Ser Ala	Phe Val
100	105	110	
Ala Glu Ser Leu Arg Ser	Gly Ile Asn Thr Val	His Phe Gly Gln Ala	
115	120	125	
Glu Ala Ala Arg Ser Leu	Gly Leu Gly Phe Ser	Asp Ile Phe Arg Ser	
130	135	140	
Ile Ile Phe Pro Gln Ala	Val Arg Ala Ala	Ile Ile Pro Leu Gly	Asn
145	150	155	160
Thr Leu Ile Ala Leu	Thr Lys Asn Thr	Ile Ala Ser Val Ile	Gly
165	170	175	
Val Gly Glu Ala Ser	Leu Leu Met Lys	Ser Thr Ile Glu Asn	His Ala
180	185	190	
Asn Met Leu Phe Val Val	Phe Ala Ile Phe	Ala Val Gly Phe	Met Ile
195	200	205	
Leu Thr Leu Pro Met Gly	Leu Gly Leu Gly	Lys Leu Ala Glu Lys	Met
210	215	220	
Ala Val Lys Lys			
225			

<210> 20  
<211> 277  
<212> PRT  
<213> Corynebacterium thermoaminogenes

<400> 20  
Val Gly Ser Val Leu Gln Glu Asn Gly Gln Leu Asp Gly Asp Lys Trp  
1 5 10 15  
Thr Pro Phe Leu Asp Pro Gln Thr Trp Thr Thr Tyr Leu Leu Pro Gly  
20 25 30  
Leu Trp Gly Thr Leu Lys Ala Ala Val Ala Ser Ile Leu Leu Ala Leu  
35 40 45  
Ile Met Gly Thr Leu Leu Gly Leu Gly Arg Ile Ser Glu Ile Arg Leu  
50 55 60  
Leu Arg Trp Phe Cys Gly Ile Ile Ile Glu Thr Phe Arg Ala Ile Pro  
65 70 75 80  
Val Leu Ile Leu Met Ile Phe Ala Tyr Gln Leu Phe Ala Arg Tyr Gln  
85 90 95  
Leu Val Pro Ser Arg Gln Leu Ala Phe Ala Ala Val Val Phe Gly Leu  
100 105 110  
Thr Met Tyr Asn Gly Ser Val Ile Ala Glu Ile Leu Arg Ser Gly Ile  
115 120 125  
Ala Ser Leu Pro Lys Gly Gln Arg Glu Ala Ala Ile Ala Leu Gly Met  
130 135 140  
Ser Thr Arg Gln Thr Thr Trp Ser Ile Leu Leu Pro Gln Ala Val Ala  
145 150 155 160  
Ala Met Leu Pro Ala Leu Ile Ala Gln Met Val Ile Ala Leu Lys Asp  
165 170 175  
Ser Ala Leu Gly Tyr Gln Ile Gly Tyr Ile Glu Val Val Arg Ser Gly  
180 185 190  
Ile Gln Ser Ala Ser Val Asn Arg Asn Tyr Leu Ala Ala Leu Ala Val  
195 200 205  
Val Ala Val Ile Met Ile Leu Ile Asn Phe Ala Leu Thr Ala Leu Ala  
210 215 220  
Glu Arg Ile Gln Arg Gln Leu Arg Ala Gly Arg Ala Arg Arg Asn Ile  
225 230 235 240  
Val Ala Lys Val Pro Glu Glu Pro Asp Gln Gly Leu Asp Thr Lys Asp  
245 250 255  
Asn Val Asn Val Asp Trp His Asp Pro Asp Tyr Lys Glu Val Lys His  
260 265 270  
Pro Gly Pro Ser Phe  
275

<210> 21  
<211> 3598  
<212> DNA  
<213> Corynebacterium thermoaminogenes

<220>  
<221> CDS  
<222> (454)..(3222)

<400> 21

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aaccggccgt gacacccttg ccatttggc agctccccc acctcaccat gtccacattt 120  
tccataatgt ggcctgttaac acccttggc tcaaggcttc cacgccccac cgggaccctc 180  
atcagcaggt gaaacagacc ctccgtcaat gctttgttaa aaagaaccgc cctttgtgcg 240  
tatccttgc tcaattgtgc gcgcactgcc accagcttc ctcaggattg aacacggtcg 300  
ggaaatcctc cccggatacc ctgcacgccc cacctcccac accgacacccg gcggggaggg 360  
ccggcacgt tttcagctgc gggtgatgga agcggtcgcc ggtccccgg tcgcataaac 420  
gaaatgaaaa acattccaac aggaggtgtg gaa atg gcc gat caa gca aaa ctt 474  
Met Ala Asp Gln Ala Lys Leu  
1 5

ggt ggc aaa ccc aca gat gac acc aac ttc gcg atg atc cgt gat ggc 522  
Gly Gly Lys Pro Thr Asp Asp Thr Asn Phe Ala Met Ile Arg Asp Gly  
10 15 20

gtt gca tct tat ttg aac gac tcc gac ccg gag gag acc aag gag tgg 570  
Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Lys Glu Trp  
25 30 35

atg gac tcc cta gac ggt cta ctg cag gat tcc tct ccg gag cgc gcc 618  
Met Asp Ser Leu Asp Gly Leu Leu Gln Asp Ser Ser Pro Glu Arg Ala  
40 45 50 55

cgt tac ctg atg ctg cgc ctg ctg gag ccg gca tcc gcc aag cgt gtc 666  
Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys Arg Val  
60 65 70

cca ctg ccc ccg atg acg tcc acc gat tac gtc aac acc atc ccc aca 714  
Pro Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile Pro Thr  
75 80 85

tcc atg gag ccc gat ttc ccg ggt gat gag gag atg gag aag cgc tac 762  
Ser Met Glu Pro Asp Phe Pro Gly Asp Glu Glu Met Glu Lys Arg Tyr  
90 95 100

cgc cgc tgg atg cgc tgg aac gcc gcc atc atg gtg cac cgt gcc cag 810  
Arg Arg Trp Met Arg Trp Asn Ala Ala Ile Met Val His Arg Ala Gln  
105 110 115

cgc ccg gga atc ggt gtg ggt ggg cac atc tcc acc tac gcc ggc gcc 858  
Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala Gly Ala  
120 125 130 135

gcc cca ctc tac gag gtc ggt ttc aac cac ttc ttc cgc ggc aag gac 906  
Ala Pro Leu Tyr Glu Val Gly Phe Asn His Phe Phe Arg Gly Lys Asp  
140 145 150

cac ccg ggt ggc ggt gac cag gtc ttc ttc cag ggt cac gcc tcc ccg 954  
His Pro Gly Gly Asp Gln Val Phe Phe Gln Gly His Ala Ser Pro  
155 160 165

ggc atg tac gcc cgc gcc ttc ctc gag ggc cgt ctc acc gag agc gat 1002  
Gly Met Tyr Ala Arg Ala Phe Leu Glu Gly Arg Leu Thr Glu Ser Asp  
170 175 180

ctg gac agc ttc cgc cag gag gtc tcc tac gaa ggt ggt ggc atc ccg 1050  
Leu Asp Ser Phe Arg Gln Glu Val Ser Tyr Glu Gly Gly Gly Ile Pro  
185 190 195

tcc tac ccg cac ccg cac ggc atg ccg gac ttc tgg gag ttc ccg acc 1098  
Ser Tyr Pro His Pro His Gly Met Pro Asp Phe Trp Glu Phe Pro Thr  
200 205 210 215

gtg tcc atg ggc ctc ggg ccc atg gat gcc atc tac cag gcg cgc ttc	1146
Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg Phe	
220 225 230	
aac cgc tac ctg cac aac cgt ggc atc aag gac acc tcg gag cag cac	1194
Asn Arg Tyr Leu His Asn Arg Gly Ile Lys Asp Thr Ser Glu Gln His	
235 240 245	
gtc tgg gca ttc ctc ggt gac ggc gag atg gat gag ccg gag tcc cgt	1242
Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser Arg	
250 255 260	
ggt ctc atc cac cag gct gcg ctg aac aac ctg gac aac ctc acc ttc	1290
Gly Leu Ile His Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr Phe	
265 270 275	
gtg atc aac tgc aac ctg cag cgt ctt gat ggc ccg gtc cgc ggt aac	1338
Val Ile Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly Asn	
280 285 290 295	
acc aag atc atc cag gaa ctc gag tcc ttc cgt ggt gcc ggc tgg	1386
Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly Trp	
300 305 310	
tcc gtc atc aag gtc atc tgg ggc cgt gag tgg gat gaa ctg ctg gag	1434
Ser Val Ile Lys Val Ile Trp Gly Arg Glu Trp Asp Glu Leu Leu Glu	
315 320 325	
aag gac cag gac ggt gct ctt gtc gag gtc atg aac aac acc tcc gac	1482
Lys Asp Gln Asp Gly Ala Leu Val Glu Val Met Asn Asn Thr Ser Asp	
330 335 340	
ggt gac tac cag acc ttc aag gcc aat gac ggt gcc tac gtc cgt gag	1530
Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg Glu	
345 350 355	
cac ttc ttc ggc cgt gac ccc cgc acc ctc aag ctc gtc gag gac atg	1578
His Phe Phe Gly Arg Asp Pro Arg Thr Leu Lys Leu Val Glu Asp Met	
360 365 370 375	
acc gac gag gag atc tgg aag ctg ccc cgt ggt ggc cat gac tac cgt	1626
Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr Arg	
380 385 390	
aag gtc tac gcc gcc tac aag cgt gcg ctg gag acc aag gac cgc ccg	1674
Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg Pro	
395 400 405	
acc gtc att ctc gcc cat acc atc aag ggc tac ggc ctg ggc cac aac	1722
Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His Asn	
410 415 420	
ttc gag ggc cgc aac gcg acc cac cag atg aag aag ctg acc ctg gat	1770
Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu Asp	
425 430 435	
gac ctg aag ctg ttc cgt gac aag cag ggt ctg ccc atc acc gat gag	1818
Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Leu Pro Ile Thr Asp Glu	
440 445 450 455	
gag ctg gag aag gat ccc tac ctg cct ccg tac tac cac ccg ggt gag	1866
Glu Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly Glu	
460 465 470	
gac gca ccg gag atc aag tac atg aag gag cgt cgc cag gcg ctc ggt	1914
Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Gln Ala Leu Gly	
475 480 485	

ggt	tac	ccg	gag	cgc	cgt	gag	aag	tac	gag	cca	ctg	cag	gtt	ccc	1962	
Gly	Phe	Leu	Pro	Glu	Arg	Arg	Glu	Lys	Tyr	Glu	Pro	Leu	Gln	Val	Pro	
490				495								500				
ccg	ctg	gac	aag	ctg	cgg	tcc	gtg	cgc	aag	ggt	tcc	ggc	aag	cag	cag	2010
Pro	Leu	Asp	Lys	Leu	Arg	Ser	Val	Arg	Lys	Gly	Ser	Gly	Lys	Gln	Gln	
505				510							515					
gtg	gcc	acc	acc	atg	gcc	acg	gtg	cgt	acc	tcc	aag	gaa	ctc	atg	cgg	2058
Val	Ala	Thr	Thr	Met	Ala	Thr	Val	Arg	Thr	Phe	Lys	Glu	Leu	Met	Arg	
520				525						530			535			
gac	aag	aac	ctg	gcc	gac	cgc	ttg	gtc	ccg	atc	atc	ccg	gat	gag	gcc	2106
Asp	Lys	Asn	Leu	Ala	Asp	Arg	Leu	Val	Pro	Ile	Ile	Pro	Asp	Glu	Ala	
540							545						550			
cgc	acc	tcc	ggc	ctg	gac	tcc	tgg	tcc	ccg	acc	ctg	aaa	atc	tac	aac	2154
Arg	Thr	Phe	Gly	Leu	Asp	Ser	Trp	Phe	Pro	Thr	Leu	Lys	Ile	Tyr	Asn	
555							560					565				
ccg	cac	gtt	cag	aac	tac	gtg	ccg	gtc	gac	cat	gac	ctc	atg	ctg	tcc	2202
Pro	His	Gly	Gln	Asn	Tyr	Val	Pro	Val	Asp	His	Asp	Leu	Met	Leu	Ser	
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tac	cgt	gag	gcc	aag	gac	ggc	cag	atc	ctg	cat	gag	ggc	atc	aac	gag	2250
Tyr	Arg	Glu	Ala	Lys	Asp	Gly	Gln	Ile	Leu	His	Glu	Gly	Ile	Asn	Glu	
585							590				595					
gcc	ggt	tcc	gtg	gca	tcg	ttt	atc	gcc	gcc	gga	acc	tcc	tac	gcc	acc	2298
Ala	Gly	Ser	Val	Ala	Ser	Phe	Ile	Ala	Ala	Gly	Thr	Ser	Tyr	Ala	Thr	
600							605			610				615		
cat	ggc	gag	gcc	atg	atc	ccg	ctg	tac	atc	tcc	tac	tcg	atg	tcc	ggc	2346
His	Gly	Glu	Ala	Met	Ile	Pro	Leu	Tyr	Ile	Phe	Tyr	Ser	Met	Phe	Gly	
620									625				630			
tcc	cag	cgc	acc	ggt	gac	ggc	atc	tgg	gcc	gca	gcc	gac	cag	atg	acg	2394
Phe	Gln	Arg	Thr	Gly	Asp	Gly	Ile	Trp	Ala	Ala	Ala	Asp	Gln	Met	Thr	
635								640					645			
cgt	ggt	tcc	ctc	ctg	ggc	gcc	acc	gcc	ggt	cgc	acc	acc	ctg	acc	ggt	2442
Arg	Gly	Phe	Leu	Leu	Gly	Ala	Thr	Ala	Gly	Arg	Thr	Thr	Leu	Thr	Gly	
650								655				660				
gag	ggc	ctc	cag	cac	atg	gat	ggc	cac	tcc	ccg	atc	ctg	gcc	tcc	acc	2490
Glu	Gly	Leu	Gln	His	Met	Asp	Gly	His	Ser	Pro	Ile	Leu	Ala	Ser	Thr	
665							670				675					
aac	ccc	ggt	gtg	gag	acc	tat	gac	ccg	gcg	tcc	tcc	tac	gag	atc	gcg	2538
Asn	Pro	Gly	Val	Glu	Thr	Tyr	Asp	Pro	Ala	Phe	Ser	Tyr	Glu	Ile	Ala	
680							685				690			695		
cac	ctg	gtc	cac	cgc	ggc	atc	gac	cgc	atg	tac	gga	ccg	ggc	aag	ggt	2586
His	Leu	Val	His	Arg	Gly	Ile	Asp	Arg	Met	Tyr	Gly	Pro	Gly	Lys	Gly	
700									705				710			
gag	aat	gtc	atc	tac	tac	ctc	acc	atc	tac	aac	gag	cca	acc	ccg	cag	2634
Glu	Asn	Val	Ile	Tyr	Tyr	Leu	Thr	Ile	Tyr	Asn	Glu	Pro	Thr	Pro	Gln	
715								720					725			
ccg	gct	gag	cct	gag	gat	ctg	gac	gtc	gag	ggc	ctg	cac	aag	ggc	atc	2682
Pro	Ala	Glu	Pro	Glu	Asp	Leu	Asp	Val	Glu	Gly	Leu	His	Lys	Gly	Ile	
730							735					740				
tac	ctc	tac	gac	aag	gcc	gcc	gag	ggt	gag	ggc	cat	gag	gcc	tcg	atc	2730
Tyr	Leu	Tyr	Asp	Lys	Ala	Ala	Glu	Gly	Glu	Gly	His	Glu	Ala	Ser	Ile	
745							750				755					

ctg	gcc	tcc	ggc	atc	ggc	atg	cag	tgg	gca	ctg	cgc	gcc	cgt	gac	atc	2778	
Leu	Ala	Ser	Gly	Ile	Gly	Met	Gln	Trp	Ala	Leu	Arg	Ala	Arg	Asp	Ile		
760				765					770						775		
ctc	gcc	gag	gat	tac	ggc	atc	cgt	gcc	aac	atc	ttc	tcc	gcc	acc	tcg	2826	
Leu	Ala	Glu	Asp	Tyr	Gly	Ile	Arg	Ala	Asn	Ile	Phe	Ser	Ala	Thr	Ser		
				780					785						790		
tgg	gtg	gag	ctg	gcc	cgc	gac	ggt	gcc	cgc	cgt	aac	ctg	gag	gcg	ctg	2874	
Trp	Val	Glu	Leu	Ala	Arg	Asp	Gly	Ala	Arg	Arg	Asn	Leu	Glu	Ala	Leu		
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cgc	aac	ccg	ggt	gcf	gat	gtc	ggt	gag	gca	ttc	gtg	acc	acc	cag	ctg	2922	
Arg	Asn	Pro	Gly	Ala	Asp	Val	Gly	Glu	Ala	Phe	Val	Thr	Thr	Gln	Leu		
				810				815							820		
aag	aag	ggt	tcc	ggc	ccc	tac	gtc	gcf	gtg	tcc	gac	ttc	gcf	acc	gac	2970	
Lys	Lys	Gly	Ser	Gly	Pro	Tyr	Val	Ala	Val	Ser	Asp	Phe	Ala	Thr	Asp		
				825				830							835		
ctg	ccg	aac	cag	atc	cgc	gag	tgg	gtt	ccc	ggt	gac	tac	atc	gtc	ctc	3018	
Leu	Pro	Asn	Gln	Ile	Arg	Glu	Trp	Val	Pro	Gly	Asp	Tyr	Ile	Val	Leu		
				840				845							855		
ggt	gcc	gac	ggc	ttc	ggt	ttc	tcc	gat	acc	cgt	ccg	gca	gcc	cgt	cgt	3066	
Gly	Ala	Asp	Gly	Phe	Gly	Phe	Ser	Asp	Thr	Arg	Pro	Ala	Ala	Arg	Arg		
				860				865							870		
tac	ttc	aac	atc	gac	gcc	gag	tcc	atc	gtc	gtg	gcf	gtc	ctg	cgc	ggc	3114	
Tyr	Phe	Asn	Ile	Asp	Ala	Glu	Ser	Ile	Val	Val	Ala	Val	Leu	Arg	Gly		
				875				880							885		
ctg	gtc	cgc	gag	ggt	gtc	atc	gat	gcc	tcc	gtg	gcf	gcf	cac	gcf	gct	3162	
Leu	Val	Arg	Glu	Gly	Val	Ile	Asp	Ala	Ser	Val	Ala	Ala	His	Ala	Ala		
				890				895							900		
gag	aag	tac	aag	ctg	tcc	gac	ccg	acg	gca	cca	cag	gtc	gat	ccg	gac	3210	
Glu	Lys	Tyr	Lys	Leu	Ser	Asp	Pro	Thr	Ala	Pro	Gln	Val	Asp	Pro	Asp		
				905				910							915		
gca	ccg	atc	gag	tagacctgct	tgtcgacgaa	aaacacccccc	gccccctcac									3262	
Ala	Pro	Ile	Glu														
				920													
atgatgaggg	gggcgggggt	gtgctcgttt	acggcgggta	cagggggta	tcagccca	3322											
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<210> 22

<211> 923

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 22

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Phe	Ala	Met	Ile	Arg	Asp	Gly	Val	Ala	Ser	Tyr	Leu	Asn	Asp	Ser	Asp	
				20					25					30		
Pro	Glu	Glu	Thr	Lys	Glu	Trp	Met	Asp	Ser	Leu	Asp	Gly	Leu	Leu	Gln	

35	40	45	
Asp Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu			
50	55	60	
Arg Ala Ser Ala Lys Arg Val Pro Leu Pro Pro Met Thr Ser Thr Asp			
65	70	75	80
Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Asp Phe Pro Gly Asp			
85	90	95	
Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Met Arg Trp Asn Ala Ala			
100	105	110	
Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His			
115	120	125	
Ile Ser Thr Tyr Ala Gly Ala Ala Pro Leu Tyr Glu Val Gly Phe Asn			
130	135	140	
His Phe Phe Arg Gly Lys Asp His Pro Gly Gly Asp Gln Val Phe			
145	150	155	160
Phe Gln Gly His Ala Ser Pro Gly Met Tyr Ala Arg Ala Phe Leu Glu			
165	170	175	
Gly Arg Leu Thr Glu Ser Asp Leu Asp Ser Phe Arg Gln Glu Val Ser			
180	185	190	
Tyr Glu Gly Gly Ile Pro Ser Tyr Pro His Pro His Gly Met Pro			
195	200	205	
Asp Phe Trp Glu Phe Pro Thr Val Ser Met Gly Leu Gly Pro Met Asp			
210	215	220	
Ala Ile Tyr Gln Ala Arg Phe Asn Arg Tyr Leu His Asn Arg Gly Ile			
225	230	235	240
Lys Asp Thr Ser Glu Gln His Val Trp Ala Phe Leu Gly Asp Gly Glu			
245	250	255	
Met Asp Glu Pro Glu Ser Arg Gly Leu Ile His Gln Ala Ala Leu Asn			
260	265	270	
Asn Leu Asp Asn Leu Thr Phe Val Ile Asn Cys Asn Leu Gln Arg Leu			
275	280	285	
Asp Gly Pro Val Arg Gly Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser			
290	295	300	
Phe Phe Arg Gly Ala Gly Trp Ser Val Ile Lys Val Ile Trp Gly Arg			
305	310	315	320
Glu Trp Asp Glu Leu Leu Glu Lys Asp Gln Asp Gly Ala Leu Val Glu			
325	330	335	
Val Met Asn Asn Thr Ser Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn			
340	345	350	
Asp Gly Ala Tyr Val Arg Glu His Phe Phe Gly Arg Asp Pro Arg Thr			
355	360	365	
Leu Lys Leu Val Glu Asp Met Thr Asp Glu Glu Ile Trp Lys Leu Pro			
370	375	380	
Arg Gly Gly His Asp Tyr Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala			
385	390	395	400
Leu Glu Thr Lys Asp Arg Pro Thr Val Ile Leu Ala His Thr Ile Lys			
405	410	415	
Gly Tyr Gly Leu Gly His Asn Phe Glu Gly Arg Asn Ala Thr His Gln			
420	425	430	
Met Lys Lys Leu Thr Leu Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln			
435	440	445	

Gly Leu Pro Ile Thr Asp Glu Glu Leu Glu Lys Asp Pro Tyr Leu Pro  
 450 455 460  
 Pro Tyr Tyr His Pro Gly Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys  
 465 470 475 480  
 Glu Arg Arg Gln Ala Leu Gly Gly Phe Leu Pro Glu Arg Arg Glu Lys  
 485 490 495  
 Tyr Glu Pro Leu Gln Val Pro Pro Leu Asp Lys Leu Arg Ser Val Arg  
 500 505 510  
 Lys Gly Ser Gly Lys Gln Gln Val Ala Thr Thr Met Ala Thr Val Arg  
 515 520 525  
 Thr Phe Lys Glu Leu Met Arg Asp Lys Asn Leu Ala Asp Arg Leu Val  
 530 535 540  
 Pro Ile Ile Pro Asp Glu Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe  
 545 550 555 560  
 Pro Thr Leu Lys Ile Tyr Asn Pro His Gly Gln Asn Tyr Val Pro Val  
 565 570 575  
 Asp His Asp Leu Met Leu Ser Tyr Arg Glu Ala Lys Asp Gly Gln Ile  
 580 585 590  
 Leu His Glu Gly Ile Asn Glu Ala Gly Ser Val Ala Ser Phe Ile Ala  
 595 600 605  
 Ala Gly Thr Ser Tyr Ala Thr His Gly Glu Ala Met Ile Pro Leu Tyr  
 610 615 620  
 Ile Phe Tyr Ser Met Phe Gly Phe Gln Arg Thr Gly Asp Gly Ile Trp  
 625 630 635 640  
 Ala Ala Ala Asp Gln Met Thr Arg Gly Phe Leu Leu Gly Ala Thr Ala  
 645 650 655  
 Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln His Met Asp Gly His  
 660 665 670  
 Ser Pro Ile Leu Ala Ser Thr Asn Pro Gly Val Glu Thr Tyr Asp Pro  
 675 680 685  
 Ala Phe Ser Tyr Glu Ile Ala His Leu Val His Arg Gly Ile Asp Arg  
 690 695 700  
 Met Tyr Gly Pro Gly Lys Gly Glu Asn Val Ile Tyr Tyr Leu Thr Ile  
 705 710 715 720  
 Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu Pro Glu Asp Leu Asp Val  
 725 730 735  
 Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr Asp Lys Ala Ala Glu Gly  
 740 745 750  
 Glu Gly His Glu Ala Ser Ile Leu Ala Ser Gly Ile Gly Met Gln Trp  
 755 760 765  
 Ala Leu Arg Ala Arg Asp Ile Leu Ala Glu Asp Tyr Gly Ile Arg Ala  
 770 775 780  
 Asn Ile Phe Ser Ala Thr Ser Trp Val Glu Leu Ala Arg Asp Gly Ala  
 785 790 795 800  
 Arg Arg Asn Leu Glu Ala Leu Arg Asn Pro Gly Ala Asp Val Gly Glu  
 805 810 815  
 Ala Phe Val Thr Thr Gln Leu Lys Lys Gly Ser Gly Pro Tyr Val Ala  
 820 825 830  
 Val Ser Asp Phe Ala Thr Asp Leu Pro Asn Gln Ile Arg Glu Trp Val  
 835 840 845  
 Pro Gly Asp Tyr Ile Val Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp

850	855	860
Thr Arg Pro Ala Ala Arg Arg Tyr Phe Asn Ile Asp Ala Glu Ser Ile		
865	870	875
Val Val Ala Val Leu Arg Gly Leu Val Arg Glu Gly Val Ile Asp Ala		880
885	890	895
Ser Val Ala Ala His Ala Ala Glu Lys Tyr Lys Leu Ser Asp Pro Thr		
900	905	910
Ala Pro Gln Val Asp Pro Asp Ala Pro Ile Glu		
915	920	

<210> 23

<211> 4013

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (319)..(3735)

<400> 23

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cggcaatggg ggtctcgggc gggggcatt ctttcacgg caaggtggtg aaattccgca	180
ggtcactccc cggccggcgg tagagaacgg agcgaaaacg gaaagcaata cgtggtttc	240
cggactggcc gttacgatgt tctgaagagt gactgccatc acccaacagg ctggccctcg	300
tcgaaaggaa caaaaact gtg gtt aca aca ccc tcc acg ctg ccg gcg	351
Val Val Thr Thr Pro Ser Thr Leu Pro Ala	
1 5 10	
ttc aaa aag atc ctg gtg gcc aac cga ggt gaa atc gcg gtg cga gca	399
Phe Lys Lys Ile Leu Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala	
15 20 25	
ttc cgc gcc gcc tac gag acc ggg gcc gca acc gtg gcc atc tac ccc	447
Phe Arg Ala Ala Tyr Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro	
30 35 40	
cgg gag gac cgt ggc tcc ttc cac cgc tcc ttc gcc tcc gag gcg gtg	495
Arg Glu Asp Arg Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val	
45 50 55	
agg atc gga acc gag ggc tca ccc gtc aag gcg tac ctc gat att gat	543
Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp	
60 65 70 75	
gag atc atc aac gcc gcc aag aag gtg aaa gcg gac gcg gtc tac ccg	591
Glu Ile Ile Asn Ala Ala Lys Lys Val Lys Ala Asp Ala Val Tyr Pro	
80 85 90	
ggg tat ggt ttc ctt tcg gaa aat gcc cag ctc gcg cgt gaa tgc gcg	639
Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala	
95 100 105	
gag aac ggc att acc ttc atc ggt ccc acc ccg gag gtg ctc gac ctc	687
Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu	
110 115 120	
acg ggc gac aag tcc aag gct gtg tcc gcc gcg aag aag gcc ggg ctg	735
Thr Gly Asp Lys Ser Lys Ala Val Ser Ala Ala Lys Lys Ala Gly Leu	

125	130	135	
ccg gtg ctg gcg gaa tcc acc ccc agc acc gac atc gat gag atc gtc			783
Pro Val Leu Ala Glu Ser Thr Pro Ser Thr Asp Ile Asp Glu Ile Val			
140 145 150 155			
aag agt gcc gag ggg cag acc tac ccg atc ttc gtc aag gcc gtc gca			831
Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala			
160 165 170			
ggt ggt ggc ggg cgt ggt atg cgg ttc gtc gag aag ccc gag gac ctg			879
Gly Gly Gly Arg Gly Met Arg Phe Val Glu Lys Pro Glu Asp Leu			
175 180 185			
cgt gag ctg gcc agg gag gcc tcc cgc gag gcg gag gcc gct ttc ggt			927
Arg Glu Leu Ala Arg Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly			
190 195 200			
gac gga tcc gtc tac gtc gaa cgg gcc gtg atc aaa ccc cag cac atc			975
Asp Gly Ser Val Tyr Val Glu Arg Ala Val Ile Lys Pro Gln His Ile			
205 210 215			
gag gtg cag atc ctc ggt gat cac acc ggc gat gtc atc cac ctg tat			1023
Glu Val Gln Ile Leu Gly Asp His Thr Gly Asp Val Ile His Leu Tyr			
220 225 230 235			
gaa cgc gac tgt tcc ctg cag cgc cgc cac cag aag gtc gtg gag atc			1071
Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile			
240 245 250			
gca cct gcc cag cac ctc gac ccg gag ctg cgc gac cgc atc tgt gcc			1119
Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala			
255 260 265			
gat gcc gtg aag ttc tgc aaa tcc atc gga tac cag ggc gcc ggc acc			1167
Asp Ala Val Lys Phe Cys Lys Ser Ile Gly Tyr Gln Gly Ala Gly Thr			
270 275 280			
gtg gag ttc ctc gtc gac gag gcg ggc aac cac gtc ttc att gag atg			1215
Val Glu Phe Leu Val Asp Glu Ala Gly Asn His Val Phe Ile Glu Met			
285 290 295			
aac ccc cgc atc cag gtg gaa cac acc gtg acc gag gag gtc acc tcc			1263
Asn Pro Arg Ile Gln Val Glu His Thr Val Thr Glu Glu Val Thr Ser			
300 305 310 315			
gtc gac ctg gtc aag gcg cag atg cac ctg gcc gcc ggt gcc acc ctg			1311
Val Asp Leu Val Lys Ala Gln Met His Leu Ala Ala Gly Ala Thr Leu			
320 325 330			
aag gaa ctg ggc ctg acc cag gac aag atc acc acc cac ggt gcc gcc			1359
Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Thr Thr His Gly Ala Ala			
335 340 345			
ctg cag tgc cgc atc acc acg gag gac ccg tcc aac aac ttc cgg ccc			1407
Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Ser Asn Asn Phe Arg Pro			
350 355 360			
gac acc ggt gtg atc acc gcc tac cgc tcc ccg ggt ggt gcg ggt gtg			1455
Asp Thr Gly Val Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val			
365 370 375			
cgt ctc gac ggc gca gcc cag ctc ggc ggc gag atc acc gca cat ttc			1503
Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe			
380 385 390 395			
gat tcc atg ctg gtc aag atg acc tgc cgc ggt tcc gat ttc gag acc			1551
Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr			

	400	405	410													
gcc	gtg	tcc	cga	1599												
Ala	Val	Ser	Arg	Ala	Gln	Arg	Ala	Leu	Ala	Glu	Phe	Asn	Val	Ser	Gly	
	415			420				425								
gtg	gcc	acc	aac	atc	ggc	tcc	ctg	cgt	gcf	ctg	ctg	cgc	gag	gaa	gac	1647
Val	Ala	Thr	Asn	Ile	Gly	Phe	Leu	Arg	Ala	Leu	Leu	Arg	Glu	Glu	Asp	
	430			435				440								
tcc	acc	aag	agg	cgc	atc	gac	acc	ggc	tcc	atc	ggc	tcc	cac	cag	cac	1695
Phe	Thr	Lys	Arg	Arg	Ile	Asp	Thr	Gly	Phe	Ile	Gly	Ser	His	Gln	His	
	445			450				455								
ctg	ctc	cag	gcc	cca	ccg	gcc	gac	gat	gag	cag	ggg	cg	atc	ctg	gaa	1743
Leu	Leu	Gln	Ala	Pro	Pro	Ala	Asp	Asp	Glu	Gln	Gly	Arg	Ile	Leu	Glu	
	460			465				470							475	
tac	ctg	gcf	gat	gtc	acc	gtg	aac	aaa	ccc	cac	ggt	gaa	cgc	ccc	gag	1791
Tyr	Leu	Ala	Asp	Val	Thr	Val	Asn	Lys	Pro	His	Gly	Glu	Arg	Pro	Glu	
	480			485				490								
aca	gcc	cgt	ccg	ata	gag	aag	ctg	ccc	gag	gtg	gag	aac	atc	ccg	ctg	1839
Thr	Ala	Arg	Pro	Ile	Glu	Lys	Leu	Pro	Glu	Val	Glu	Asn	Ile	Pro	Leu	
	495			500				505								
cca	cgc	ggc	tcc	cgc	gac	cgc	ctg	aag	cag	ctc	ggc	ccg	gag	ggt	tcc	1887
Pro	Arg	Gly	Ser	Arg	Asp	Arg	Leu	Lys	Gln	Leu	Gly	Pro	Glu	Gly	Phe	
	510			515				520								
gcc	cgc	gat	ctg	cgc	gaa	cag	gat	gcc	ctg	gcc	gtc	acc	gac	acc	acc	1935
Ala	Arg	Asp	Leu	Arg	Glu	Gln	Asp	Ala	Leu	Ala	Val	Thr	Asp	Thr	Thr	
	525			530				535								
tcc	cgc	gat	gcc	cac	cag	tcc	ctc	ctg	gcc	acc	cgc	gtg	cgc	tcc	tcc	1983
Phe	Arg	Asp	Ala	His	Gln	Ser	Leu	Leu	Ala	Thr	Arg	Val	Arg	Ser	Phe	
	540			545				550							555	
gcg	ctg	acc	ccg	gcf	ccg	gcc	gtc	gca	aag	ctc	acc	ccc	gag	ctg	2031	
Ala	Leu	Thr	Pro	Ala	Ala	Arg	Ala	Val	Ala	Lys	Leu	Thr	Pro	Glu	Leu	
	560			565				570								
ctg	tcg	gtg	gag	gcc	tgg	ggc	ggt	gcc	acc	tac	gac	gtg	gcc	atg	cgc	2079
Leu	Ser	Val	Glu	Ala	Trp	Gly	Gly	Ala	Thr	Tyr	Asp	Val	Ala	Met	Arg	
	575			580				585								
tcc	ctc	tcc	gag	gat	ccg	tgg	gca	cgc	ctg	gat	gag	ctg	cgt	gag	gcf	2127
Phe	Leu	Phe	Glu	Asp	Pro	Trp	Ala	Arg	Leu	Asp	Glu	Leu	Arg	Glu	Ala	
	590			595				600								
atg	ccg	aat	gtg	aac	atc	cag	atg	ctg	ctg	cgt	ggt	cgc	aac	acc	gtc	2175
Met	Pro	Asn	Val	Asn	Ile	Gln	Met	Leu	Leu	Arg	Gly	Arg	Asn	Thr	Val	
	605			610				615								
ggg	tac	acc	ccg	tac	ccc	gat	tcg	gtg	tgc	cgc	gcf	ttt	gtg	cag	gag	2223
Gly	Tyr	Thr	Pro	Tyr	Pro	Asp	Ser	Val	Cys	Arg	Ala	Phe	Val	Gln	Glu	
	620			625				630							635	
gcc	gcc	aag	tcc	ggt	gtg	gac	atc	tcc	cgc	atc	tcc	gac	gcf	ctc	aac	2271
Ala	Ala	Lys	Ser	Gly	Val	Asp	Ile	Phe	Arg	Ile	Phe	Asp	Ala	Leu	Asn	
	640			645				650								
gac	atc	tcc	cag	atg	cgc	ccg	gcc	atc	gac	gcc	gtc	ctg	gag	acc	ggc	2319
Asp	Ile	Ser	Gln	Met	Arg	Pro	Ala	Ile	Asp	Ala	Val	Leu	Glu	Thr	Gly	
	655			660				665								
acc	agt	gtt	gcc	gag	gtc	gcc	atg	gcf	tac	tcc	ggt	gac	ctg	tcc	aat	2367
Thr	Ser	Val	Ala	Glu	Val	Ala	Met	Ala	Tyr	Ser	Gly	Asp	Leu	Ser	Asn	

	670	675	680		
ccg	ggg	gag	aag	ctc tac acc ctg gac tac tac ctg aac ctg gcc gag	2415
Pro	Gly	Glu	Lys	Leu Tyr Thr Leu Asp Tyr Tyr Leu Asn Leu Ala Glu	
685	690	695			
cag	atc	gtc	gac	tcc ggt gca cac atc ctg gcc atc aag gac atg gcc	2463
Gln	Ile	Val	Asp	Ser Gly Ala His Ile Leu Ala Ile Lys Asp Met Ala	
700	705	710	715		
ggc	ctg	ctg	cgc	cgc gcc gcg ccc aaa ctg gtc acc gcc ctg cgc	2511
Gly	Leu	Leu	Arg	Arg Ala Ala Ala Pro Lys Leu Val Thr Ala Leu Arg	
	720	725	730		
cgt	gaa	ttc	gac	ctg ccc gtg cat gtc cac acc cac gac acc gcc ggc	2559
Arg	Glu	Phe	Asp	Leu Pro Val His Val His Thr His Asp Thr Ala Gly	
	735	740	745		
ggt	cag	ctg	gcc	acc tac ctg gcc gcc aac gcc ggg gcc gat gcc	2607
Gly	Gln	Leu	Ala	Thr Tyr Leu Ala Ala Ala Asn Ala Gly Ala Asp Ala	
	750	755	760		
gtc	gac	gcc	gcc	tcc gca ccc ctg tcc ggt acc acc tcc cag ccg tcg	2655
Val	Asp	Ala	Ala	Ser Ala Pro Leu Ser Gly Thr Thr Ser Gln Pro Ser	
	765	770	775		
atg	tcc	gct	ctg	gtt gcc gcg ttt gcg cac acc cga cgc gac acc ggc	2703
Met	Ser	Ala	Leu	Val Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly	
	780	785	790	795	
ctc	aac	ctg	cag	gcc gtc tcc gac ctg gaa ccg tac tgg gag gcg gtc	2751
Leu	Asn	Leu	Gln	Ala Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val	
	800	805	810		
cgc	gga	ctg	tac	ctg ccg ttt gaa tcc ggc acc ccg ggc ccg acc gga	2799
Arg	Gly	Leu	Tyr	Leu Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly	
	815	820	825		
cgc	gtt	tac	cgc	cac gag atc ccc ggc ggt cag ctg tcc aac ctg cgt	2847
Arg	Val	Tyr	Arg	His Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg	
	830	835	840		
gcc	cag	gcc	gtt	gca ctg ggt ctg gcc gac cgc ttc gag ctc atc gag	2895
Ala	Gln	Ala	Val	Ala Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu	
	845	850	855		
gac	tac	tac	gcg	gcc gtc aac gag atg ctg ggt cgt ccg acc aag gtc	2943
Asp	Tyr	Tyr	Ala	Ala Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val	
	860	865	870	875	
acc	ccg	tcc	tcc	aag gtt gtc ggt gac ctc gca ctg cac ctc gtc ggt	2991
Thr	Pro	Ser	Ser	Lys Val Val Gly Asp Leu Ala Leu His Leu Val Gly	
	880	885	890		
gcc	ggt	gtg	agc	ccg gag gat ttc gcc gac gat ccg cag aag tac gac	3039
Ala	Gly	Val	Ser	Pro Glu Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp	
	895	900	905		
atc	ccc	gat	tcg	gtc atc gcc ttc ctc cgc ggc gaa ctg ggt acc acc cct	3087
Ile	Pro	Asp	Ser	Val Ile Ala Phe Leu Arg Gly Glu Leu Gly Thr Pro	
	910	915	920		
ccc	ggt	ggc	tgg	ccc gaa ccg ctg cgc acc cgt gca ctc gag ggt cgc	3135
Pro	Gly	Gly	Trp	Pro Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg	
	925	930	935		
tcc	cag	ggt	aag	gcc ccg ctg gcg gag atc ccc gcc gag gag cag gcc	3183
Ser	Gln	Gly	Lys	Ala Pro Leu Ala Glu Ile Pro Ala Glu Glu Gln Ala	

940	945	950	955	
cac ctg gat tcc gat gat tcc gcg gag cgt cgc ggc acc ctc aac cgc				3231
His Leu Asp Ser Asp Asp Ser Ala Glu Arg Arg Gly Thr Leu Asn Arg				
960	965	970		
ctg ctg ttc ccg aag ccg acc gag gag ttc ctt gag cac cgt cgc cgc				3279
Leu Leu Phe Pro Lys Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg				
975	980	985		
ttc ggc aac acc tcc gcc ctg gat gac cgc gag ttc ttc tac ggc ttg				3327
Phe Gly Asn Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu				
990	995	1000		
aag gag gga cgt gag gag ctg atc cga ctg acc ggt gtg tcc acc ccg				3375
Lys Glu Gly Arg Glu Glu Leu Ile Arg Leu Thr Gly Val Ser Thr Pro				
1005	1010	1015		
atg gtg gtc cgc ctg gat gcg gtg tcc gaa ccg gat gac aaa ggc atg				3423
Met Val Val Arg Leu Asp Ala Val Ser Glu Pro Asp Asp Lys Gly Met				
1020	1025	1030	1035	
cgc aac gtg gtg gtc aac gtc aac ggc cag atc cgc ccg atc aag gtg				3471
Arg Asn Val Val Asn Val Asn Gly Gln Ile Arg Pro Ile Lys Val				
1040	1045	1050		
cgc gac cgt tcc gtg gag tcc gtc acc gcc acc gcg gag aag gcc gat				3519
Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu Lys Ala Asp				
1055	1060	1065		
gcc acc aac aag ggc cat gtc gcc gca cca ttc gcc ggt gtg gtc acc				3567
Ala Thr Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly Val Val Thr				
1070	1075	1080		
gtg acc gtc gcc gag ggt gat gag atc aag gct ggc gac gcc gtc gcc				3615
Val Thr Val Ala Glu Gly Asp Glu Ile Lys Ala Gly Asp Ala Val Ala				
1085	1090	1095		
atc att gag gcc atg aag atg gag gcc acc atc acc gcg cct gtc gac				3663
Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala Pro Val Asp				
1100	1105	1110	1115	
ggt gtc atc gac cgc gtc gtg ccc gcc acc aag gtc gag ggc				3711
Gly Val Ile Asp Arg Val Val Pro Ala Ala Thr Lys Val Glu Gly				
1120	1125	1130		
ggc gac ctc atc gtg gtc gtg tcc tagcgactga gagccacaac ccgtccggg				3765
Gly Asp Leu Ile Val Val Ser				
1135				
tgccttgtta tcaaacctccc cctgatgatg ttctcagggg gaggctctac gtacctcacc				3825
gtgacgggtgc atgtataatcg tcctgctgga gagaatgctc caggttagaa cgccaaccac				3885
cccactccgt gatgtcccggt gctgatccca ggcaggccgg ttggaaaagaa aaaccagtga				3945
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<213> Corynebacterium thermoaminogenes

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     20                 25                                 30  
 Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly  
     35                 40                                 45  
 Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu  
     50                 55                                 60  
 Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Asn Ala  
     65                 70                                 75                         80  
 Ala Lys Lys Val Lys Ala Asp Ala Val Tyr Pro Gly Tyr Gly Phe Leu  
     85                 90                                 95  
 Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr  
     100                 105                                 110  
 Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser  
     115                 120                                 125  
 Lys Ala Val Ser Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu  
     130                 135                                 140  
 Ser Thr Pro Ser Thr Asp Ile Asp Glu Ile Val Lys Ser Ala Glu Gly  
     145                 150                                 155                         160  
 Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Arg  
     165                 170                                 175  
 Gly Met Arg Phe Val Glu Lys Pro Glu Asp Leu Arg Glu Leu Ala Arg  
     180                 185                                 190  
 Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ser Val Tyr  
     195                 200                                 205  
 Val Glu Arg Ala Val Ile Lys Pro Gln His Ile Glu Val Gln Ile Leu  
     210                 215                                 220  
 Gly Asp His Thr Gly Asp Val Ile His Leu Tyr Glu Arg Asp Cys Ser  
     225                 230                                 235                         240  
 Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His  
     245                 250                                 255  
 Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe  
     260                 265                                 270  
 Cys Lys Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val  
     275                 280                                 285  
 Asp Glu Ala Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln  
     290                 295                                 300  
 Val Glu His Thr Val Thr Glu Glu Val Thr Ser Val Asp Leu Val Lys  
     305                 310                                 315                         320  
 Ala Gln Met His Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu  
     325                 330                                 335  
 Thr Gln Asp Lys Ile Thr Thr His Gly Ala Ala Leu Gln Cys Arg Ile  
     340                 345                                 350  
 Thr Thr Glu Asp Pro Ser Asn Asn Phe Arg Pro Asp Thr Gly Val Ile  
     355                 360                                 365  
 Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala  
     370                 375                                 380  
 Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val  
     385                 390                                 395                         400  
 Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ser Arg Ala  
     405                 410                                 415  
 Gln Arg Ala Leu Ala Glu Phe Asn Val Ser Gly Val Ala Thr Asn Ile

	420	425	430
Gly Phe Leu Arg Ala Leu Leu Arg	Glu Glu Asp Phe Thr Lys Arg Arg		
435	440	445	
Ile Asp Thr Gly Phe Ile Gly Ser His Gln His	Leu Leu Gln Ala Pro		
450	455	460	
Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Glu Tyr Leu Ala Asp Val			
465	470	475	480
Thr Val Asn Lys Pro His Gly Glu Arg Pro Glu Thr Ala Arg Pro Ile			
485	490	495	
Glu Lys Leu Pro Glu Val Glu Asn Ile Pro Leu Pro Arg Gly Ser Arg			
500	505	510	
Asp Arg Leu Lys Gln Leu Gly Pro Glu Gly Phe Ala Arg Asp Leu Arg			
515	520	525	
Glu Gln Asp Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala His			
530	535	540	
Gln Ser Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Thr Pro Ala			
545	550	555	560
Ala Arg Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala			
565	570	575	
Trp Gly Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp			
580	585	590	
Pro Trp Ala Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn			
595	600	605	
Ile Gln Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr			
610	615	620	
Pro Asp Ser Val Cys Arg Ala Phe Val Gln Glu Ala Ala Lys Ser Gly			
625	630	635	640
Val Asp Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Ile Ser Gln Met			
645	650	655	
Arg Pro Ala Ile Asp Ala Val Leu Glu Thr Gly Thr Ser Val Ala Glu			
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Val Ala Met Ala Tyr Ser Gly Asp Leu Ser Asn Pro Gly Glu Lys Leu			
675	680	685	
Tyr Thr Leu Asp Tyr Tyr Leu Asn Leu Ala Glu Gln Ile Val Asp Ser			
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Gly Ala His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Arg			
705	710	715	720
Ala Ala Ala Pro Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu			
725	730	735	
Pro Val His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr			
740	745	750	
Tyr Leu Ala Ala Ala Asn Ala Gly Ala Asp Ala Val Asp Ala Ala Ser			
755	760	765	
Ala Pro Leu Ser Gly Thr Thr Ser Gln Pro Ser Met Ser Ala Leu Val			
770	775	780	
Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Asn Leu Gln Ala			
785	790	795	800
Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu			
805	810	815	
Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His			
820	825	830	

Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Val Ala  
 835 840 845  
 Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Tyr Tyr Ala Ala  
 850 855 860  
 Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys  
 865 870 875 880  
 Val Val Gly Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Ser Pro  
 885 890 895  
 Glu Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val  
 900 905 910  
 Ile Ala Phe Leu Arg Gly Glu Leu Gly Thr Pro Pro Gly Gly Trp Pro  
 915 920 925  
 Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg Ser Gln Gly Lys Ala  
 930 935 940  
 Pro Leu Ala Glu Ile Pro Ala Glu Glu Gln Ala His Leu Asp Ser Asp  
 945 950 955 960  
 Asp Ser Ala Glu Arg Arg Gly Thr Leu Asn Arg Leu Leu Phe Pro Lys  
 965 970 975  
 Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser  
 980 985 990  
 Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu Lys Glu Gly Arg Glu  
 995 1000 1005  
 Glu Leu Ile Arg Leu Thr Gly Val Ser Thr Pro Met Val Val Arg Leu  
 1010 1015 1020  
 Asp Ala Val Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Val  
 1025 1030 1035 1040  
 Asn Val Asn Gly Gln Ile Arg Pro Ile Lys Val Arg Asp Arg Ser Val  
 1045 1050 1055  
 Glu Ser Val Thr Ala Thr Ala Glu Lys Ala Asp Ala Thr Asn Lys Gly  
 1060 1065 1070  
 His Val Ala Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu  
 1075 1080 1085  
 Gly Asp Glu Ile Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met  
 1090 1095 1100  
 Lys Met Glu Ala Thr Ile Thr Ala Pro Val Asp Gly Val Ile Asp Arg  
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 Val Val Ser

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<400> 25

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 acc gtg aat gaa ctt ctc cgt gac gat atc cgt tat ctc ggc cggt atc 108  
     Val Asn Glu Leu Leu Arg Asp Asp Ile Arg Tyr Leu Gly Arg Ile  
     1                   5                   10                   15  
 ctg ggc gag gtg atc tcc gag cag gag ggc cac cat gtc ttc gaa ctg 156  
 Leu Gly Glu Val Ile Ser Glu Gln Glu Gly His His Val Phe Glu Leu  
     20                   25                   30  
 gtt gaa cgc gcc cgc cggt acc tcc ttc gac atc gcc aag gga cgc gcg 204  
 Val Glu Arg Ala Arg Arg Thr Ser Phe Asp Ile Ala Lys Gly Arg Ala  
     35                   40                   45  
 gag atg gac agt ctg gtg gag gtg ttc gct ggc atc gac ccg gag gac 252  
 Glu Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp  
     50                   55                   60  
 gcc acg ccc gtg gcc cga gcc ttc acc cat ttc gcc ctg ttg gcc aac 300  
 Ala Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn  
     65                   70                   75  
 ctc gcg gag gat ttg cat gac gca gcc cag cggt gaa cag gcc ctg aac 348  
 Leu Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn  
     80                   85                   90                   95  
 tcg ggt gag ccc gcg ccg gac agc acc ctc gag gcc acc tgg gtg aaa 396  
 Ser Gly Glu Pro Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys  
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 ctg gat gat gcc ggg gtg ggc agc ggt gag gtc gcc gcg gtg atc cgc 444  
 Leu Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg  
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 aat gcg ctc gtc gcc ccg gtg ctc acc gcg cac ccg acg gaa acc cga 492  
 Asn Ala Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg  
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 cgt cgt acc gtg ttc gac gcg cag aag cac atc acc gcc ctg atg gag 540  
 Arg Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala Leu Met Glu  
     145                   150                   155  
 gaa cgc cac ctc ctc ctg gcg ctg ccc acg cat gcc cggt acc cag tcc 588  
 Glu Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser  
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 aag ctg gat gac atc gag cgc aac atc cggt cga cggt atc acg atc ctg 636  
 Lys Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu  
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 tgg cag acg gcc ctc atc cgt gtg gcc cgt ccc cgc atc gag gat gag 684  
 Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu  
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 gtc gag gtt gga ctg cgc tac tac aag ctc agc ctg ttg gcc gag atc 732  
 Val Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile  
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 ccc cgc atc aat cat gat gtg acc gtg gaa ctg gcc cggt ttc ggc 780  
 Pro Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly  
     225                   230                   235  
 ggg gat atc ccc acc acg gcg atg gtc agg ccg gga tcc tgg atc ggc 828  
 Gly Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly  
     240                   245                   250                   255  
 ggg gac cat gat ggc aac ccc ttc gtc acc gcg gag act gtc acc tac 876  
 Gly Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr

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gcc acc cat cgg gcc gcg gag acc gtg ctc aag tac tac gtc aag caa				924
Ala Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Val Lys Gln				
275 280 285				
ctg cac gcc ctg gaa cac gaa ctc agt ctc tcc gac cggt atg aac gtc				972
Leu His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Val				
290 295 300				
atc agc gat gag ctg cgt gtg ctt gcc gat gcc ggc cag aat gac atg				1020
Ile Ser Asp Glu Leu Arg Val Leu Ala Asp Ala Gly Gln Asn Asp Met				
305 310 315				
ccc agc cggt gtt gat gaa ccc tac cggt cggt gcc atc cac ggc atg cgt				1068
Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Ile His Gly Met Arg				
320 325 330 335				
ggc cggt atg ctg gcc acc acg gcc gcc ctg atc ggt gag gag ggc gtc				1116
Gly Arg Met Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu Glu Ala Val				
340 345 350				
gag ggc acc tgg ttc aag acc ttc acg ccc tat acc gat acc cac gag				1164
Glu Gly Thr Trp Phe Lys Thr Phe Thr Pro Tyr Thr Asp Thr His Glu				
355 360 365				
tcc aaa cgc gac ctc gat atc gtg gat ggt tcc ctg aga atg tcc cggt				1212
Phe Lys Arg Asp Leu Asp Ile Val Asp Gly Ser Leu Arg Met Ser Arg				
370 375 380				
gat gac atc atc gcc gat gac cgt ctg gcc atg ctg cgc tcg gcc ctg				1260
Asp Asp Ile Ile Ala Asp Asp Arg Leu Ala Met Leu Arg Ser Ala Leu				
385 390 395				
gac agc ttc ggg ttc aac ctc tac tcc ctg gat ctg cgc cag aat tcc				1308
Asp Ser Phe Gly Phe Asn Leu Tyr Ser Leu Asp Leu Arg Gln Asn Ser				
400 405 410 415				
gac ggt ttc gag gat gtc ctc acc gaa ttg ttc gcc acc gcc cag acc				1356
Asp Gly Phe Glu Asp Val Leu Thr Glu Leu Phe Ala Thr Ala Gln Thr				
420 425 430				
gag aag aac tac cgc ggg ttg acg gag gcg gag aag ctg gac ctg ctg				1404
Glu Lys Asn Tyr Arg Gly Leu Thr Glu Ala Glu Lys Leu Asp Leu Leu				
435 440 445				
atc cgc gaa ctg agc aca ccc cgc ccgt ctc atc ccgt cac ggg gac ccgt				1452
Ile Arg Glu Leu Ser Thr Pro Arg Pro Leu Ile Pro His Gly Asp Pro				
450 455 460				
gac tac tcc gag gcc acc aac cgt gaa ctg ggg att ttt tcg aag gcc				1500
Asp Tyr Ser Glu Ala Thr Asn Arg Glu Leu Gly Ile Phe Ser Lys Ala				
465 470 475				
gcg gag gcc gtg cgt aaa ttc ggt cct ctc atg gtg ccgt cac tgc atc				1548
Ala Glu Ala Val Arg Lys Phe Gly Pro Leu Met Val Pro His Cys Ile				
480 485 490 495				
atc tcc atg gcc tct tcc gtc acg gac atc ctc gaa ccgt atg gtg ctg				1596
Ile Ser Met Ala Ser Ser Val Thr Asp Ile Leu Glu Pro Met Val Leu				
500 505 510				
ctc aag gag ttc ggt ctg atc cgg gcc aac ggg aag aac ccgt acg ggc				1644
Leu Lys Glu Phe Gly Leu Ile Arg Ala Asn Gly Lys Asn Pro Thr Gly				
515 520 525				
agc gtc gac gtg atc ccgt ctg ttc gag acg atc gat gac ctc cag cgt				1692
Ser Val Asp Val Ile Pro Leu Phe Glu Thr Ile Asp Asp Leu Gln Arg				

530	535	540	
ggc gcg ggc atc ctg gag gaa ttg tgg gac atc gac	ctc tac cgc aat		1740
Gly Ala Gly Ile Leu Glu Glu Leu Trp Asp Ile Asp	Leu Tyr Arg Asn		
545	550	555	
tac ctt gag cag cg gac aac gtc cag gag gtc atg	ctg ggg tat tcc		1788
Tyr Leu Glu Gln Arg Asp Asn Val Gln Glu Val	Met Leu Gly Tyr Ser		
560	565	570	575
gac tcc aac aag gac ggc ggg tac ttc gcc gcc aac	tgg gcg ctt tac		1836
Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn	Trp Ala Leu Tyr		
580	585	590	
gac gcg gag tta cgc ctg gtc gaa cta tgc cgg ggc	cgt aat gtc aag		1884
Asp Ala Glu Leu Arg Leu Val Glu Leu Cys Arg Gly	Arg Asn Val Lys		
595	600	605	
ctc cgt ctc ttc cac ggt cgt ggt ggc acg gtg ggt	cgt ggc ggt ggc		1932
Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly	Arg Gly Gly Gly		
610	615	620	
ccc tcc tat gat gcg atc ctg gcc cag ccc aag ggc	gcg gtc cgg ggt		1980
Pro Ser Tyr Asp Ala Ile Leu Ala Gln Pro Lys Gly	Ala Val Arg Gly		
625	630	635	
gcg gtg cg ggt act gaa cag ggc gag atc atc tcc	gcg aag tac ggt		2028
Ala Val Arg Val Thr Glu Gln Gly Glu Ile Ile Ser	Ala Lys Tyr Gly		
640	645	650	655
aac ccg gat acg gca cgc cgc aac ctt gag gcc ctg	gtg tcc gcg acg		2076
Asn Pro Asp Thr Ala Arg Arg Asn Leu Glu Ala Leu	Val Ser Ala Thr		
660	665	670	
ctg gag gca tcg ctt ctg gat gat gtg gaa ctg ccc	aat cgg gaa cgc		2124
Leu Glu Ala Ser Leu Leu Asp Asp Val Glu Leu Pro	Asn Arg Glu Arg		
675	680	685	
gcg cac cag atc atg ggg gag atc tcg gag ttg agc	ttc cgc agg tac		2172
Ala His Gln Ile Met Gly Glu Ile Ser Glu Leu Ser	Phe Arg Arg Tyr		
690	695	700	
tca tca ctg gtc cat gag gat ccc gga ttc atc cag	tac ttc acc cag		2220
Ser Ser Leu Val His Glu Asp Pro Gly Phe Ile Gln	Tyr Phe Thr Gln		
705	710	715	
tcc acc ccc ctg cag gag atc gga tcc ctc aac atc	ggt tcc cga ccc		2268
Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile	Gly Ser Arg Pro		
720	725	730	735
tcc tca cgt aaa cag acc aac acg gtg gag gat	ctg cgt gcc atc ccg		2316
Ser Ser Arg Lys Gln Thr Asn Thr Val Glu Asp Leu	Arg Ala Ile Pro		
740	745	750	
tgg gtg ctc agc tgg tcc cag tcc cgt gtc atg	ctg ccg ggc tgg ttc		2364
Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu	Pro Gly Trp Phe		
755	760	765	
ggt gtg ggt acc gca ctg cgt gag tgg atc ggt gag	ggg gag ggg gct		2412
Gly Val Gly Thr Ala Leu Arg Glu Trp Ile Gly Glu	Gly Glu Gly Ala		
770	775	780	
gcg gag cgc atc gcg gag ctg cag gaa ctc aac cgg	tgc tgg ccg ttc		2460
Ala Glu Arg Ile Ala Glu Leu Gln Glu Leu Asn Arg	Cys Trp Pro Phe		
785	790	795	
tcc acc tcg gtg ctg gac aac atg gcc cag gtg atg	agc aag gcg gaa		2508
Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met	Ser Lys Ala Glu		

800	805	810	815	2556
ctg cgc ctg gcc agg ttg tac gcc gat ctc atc ccg gat cgc gag gtg				
Leu Arg Leu Ala Arg Leu Tyr Ala Asp	Leu	Ile	Pro	Asp Arg Glu Val
820	825	830		
gag gac cgg atc tat gag acc atc ttc ggg gag tat ttc ctg acc aag				2604
Ala Asp Arg Ile Tyr Glu Thr Ile Phe Gly Glu Tyr Phe Leu Thr Lys				
835	840	845		
gag atg ttc tgc acc atc acc ggt tcc cag gac ctg ctc gat gac aac				2652
Glu Met Phe Cys Thr Ile Thr Gly Ser Gln Asp Leu Leu Asp Asp Asn				
850	855	860		
ccg gcg ctg gcg cga tcg gtg cgc agt cgg ttc ccg tac ctg ctg ccg				2700
Pro Ala Leu Ala Arg Ser Val Arg Ser Arg Phe Pro Tyr Leu Leu Pro				
865	870	875		
ctc aat gtc atc cag gtg gag atg atg cgc cgg tac cgg tcc ggt gat				2748
Leu Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Ser Gly Asp				
880	885	890	895	
gag ggc acg gct gtc cca cgt aat atc cgc ctg acc atg aat gga ttg				2796
Glu Gly Thr Ala Val Pro Arg Asn Ile Arg Leu Thr Met Asn Gly Leu				
900	905	910		
tcc acg gcc ctg cgc aac tcg ggt tagggcgcca gacgccccgg gaacccgcac				2850
Ser Thr Ala Leu Arg Asn Ser Gly				
915				
cctgtgtata ctgtctaaag ttgccccgtg tcatccgggc gtgatggata gacaacttaa				2910
cggcaaagga ttctccccac atggcactga cgcttcaa at cgtcctcg tt ctcggccagcg				2970
tgctcatgac ggtcttcgtc ctgctgcaca agggtaaggg cggaggtctg tcaagcctct				3030
tcgggtgggt ggccgtcc aacctctccg gttccacgggt ggtggagaag aacctggacc				3090
gcgtcaccat cctgaccgca gtcatctgt tgatctgc at tgtcgcgtc aacctcatcc				3150
aggcgtactc ctagcacctg atcttcaag gcctgccc tt cggggcaggc ctttttgca				3210
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<212> PRT  
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 1 5 Val Asn Glu Leu Leu Arg Asp Asp Ile Arg Tyr Leu Gly Arg Ile Leu  
 Gly Glu Val Ile Ser Glu Gln Glu Gly His His Val Phe Glu Leu Val  
 20 25 30 Gly Glu Val Ile Ser Glu Gln Glu Gly His His Val Phe Glu Leu Val  
 Glu Arg Ala Arg Arg Thr Ser Phe Asp Ile Ala Lys Gly Arg Ala Glu  
 45  
 35 40 Glu Arg Ala Arg Arg Thr Ser Phe Asp Ile Ala Lys Gly Arg Ala Glu  
 Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp Ala  
 60  
 50 55 Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp Ala  
 Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn Leu  
 80  
 65 70 Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn Leu  
 Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn Ser  
 95  
 85 90 Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn Ser  
 Gly Glu Pro Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys Leu  
 110  
 100 105 Gly Glu Pro Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys Leu

Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg Asn  
 115 120 125  
 Ala Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg Arg  
 130 135 140  
 Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala Leu Met Glu Glu  
 145 150 155 160  
 Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser Lys  
 165 170 175  
 Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu Trp  
 180 185 190  
 Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu Val  
 195 200 205  
 Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile Pro  
 210 215 220  
 Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly Gly  
 225 230 235 240  
 Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly Gly  
 245 250 255  
 Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr Ala  
 260 265 270  
 Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Val Lys Gln Leu  
 275 280 285  
 His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Val Ile  
 290 295 300  
 Ser Asp Glu Leu Arg Val Leu Ala Asp Ala Gly Gln Asn Asp Met Pro  
 305 310 315 320  
 Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Ile His Gly Met Arg Gly  
 325 330 335  
 Arg Met Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu Glu Ala Val Glu  
 340 345 350  
 Gly Thr Trp Phe Lys Thr Phe Thr Pro Tyr Thr Asp Thr His Glu Phe  
 355 360 365  
 Lys Arg Asp Leu Asp Ile Val Asp Gly Ser Leu Arg Met Ser Arg Asp  
 370 375 380  
 Asp Ile Ile Ala Asp Asp Arg Leu Ala Met Leu Arg Ser Ala Leu Asp  
 385 390 395 400  
 Ser Phe Gly Phe Asn Leu Tyr Ser Leu Asp Leu Arg Gln Asn Ser Asp  
 405 410 415  
 Gly Phe Glu Asp Val Leu Thr Glu Leu Phe Ala Thr Ala Gln Thr Glu  
 420 425 430  
 Lys Asn Tyr Arg Gly Leu Thr Glu Ala Glu Lys Leu Asp Leu Leu Ile  
 435 440 445  
 Arg Glu Leu Ser Thr Pro Arg Pro Leu Ile Pro His Gly Asp Pro Asp  
 450 455 460  
 Tyr Ser Glu Ala Thr Asn Arg Glu Leu Gly Ile Phe Ser Lys Ala Ala  
 465 470 475 480  
 Glu Ala Val Arg Lys Phe Gly Pro Leu Met Val Pro His Cys Ile Ile  
 485 490 495  
 Ser Met Ala Ser Ser Val Thr Asp Ile Leu Glu Pro Met Val Leu Leu  
 500 505 510  
 Lys Glu Phe Gly Leu Ile Arg Ala Asn Gly Lys Asn Pro Thr Gly Ser

515	520	525	
Val Asp Val Ile Pro Leu Phe Glu Thr Ile Asp Asp	Leu Gln Arg Gly		
530	535	540	
Ala Gly Ile Leu Glu Glu Leu Trp Asp Ile Asp	Leu Tyr Arg Asn Tyr		
545	550	555	560
Leu Glu Gln Arg Asp Asn Val Gln Glu Val	Met Leu Gly Tyr Ser Asp		
565	570	575	
Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn Trp Ala	Leu Tyr Asp		
580	585	590	
Ala Glu Leu Arg Leu Val Glu Leu Cys Arg Gly Arg Asn Val	Lys Leu		
595	600	605	
Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Pro			
610	615	620	
Ser Tyr Asp Ala Ile Leu Ala Gln Pro Lys Gly Ala Val Arg Gly Ala			
625	630	635	640
Val Arg Val Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn			
645	650	655	
Pro Asp Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu			
660	665	670	
Glu Ala Ser Leu Leu Asp Asp Val Glu Leu Pro Asn Arg Glu Arg Ala			
675	680	685	
His Gln Ile Met Gly Glu Ile Ser Glu Leu Ser Phe Arg Arg Tyr Ser			
690	695	700	
Ser Leu Val His Glu Asp Pro Gly Phe Ile Gln Tyr Phe Thr Gln Ser			
705	710	715	720
Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser			
725	730	735	
Ser Arg Lys Gln Thr Asn Thr Val Glu Asp Leu Arg Ala Ile Pro Trp			
740	745	750	
Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly			
755	760	765	
Val Gly Thr Ala Leu Arg Glu Trp Ile Gly Glu Gly Glu Gly Ala Ala			
770	775	780	
Glu Arg Ile Ala Glu Leu Gln Glu Leu Asn Arg Cys Trp Pro Phe Phe			
785	790	795	800
Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu			
805	810	815	
Arg Leu Ala Arg Leu Tyr Ala Asp Leu Ile Pro Asp Arg Glu Val Ala			
820	825	830	
Asp Arg Ile Tyr Glu Thr Ile Phe Gly Glu Tyr Phe Leu Thr Lys Glu			
835	840	845	
Met Phe Cys Thr Ile Thr Gly Ser Gln Asp Leu Leu Asp Asp Asn Pro			
850	855	860	
Ala Leu Ala Arg Ser Val Arg Ser Arg Phe Pro Tyr Leu Leu Pro Leu			
865	870	875	880
Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Ser Gly Asp Glu			
885	890	895	
Gly Thr Ala Val Pro Arg Asn Ile Arg Leu Thr Met Asn Gly Leu Ser			
900	905	910	
Thr Ala Leu Arg Asn Ser Gly			
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<210> 27  
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 <212> DNA  
 <213> Corynebacterium thermoaminogenes

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 aatccaagta gtatggtaa agtaacttgg ggtattgctc aagcacttat cgcccttgta 120  
 ttattattag ctggtggcgg agatgaaact aaagctctca acgcaattca gagtggcgct 180  
 attattatgt cgtttccatt ctccttgta gtcattaa tgcattaa tgcattaa acacagatta 240  
 gatgctaata aagaacgtaa attcttagga ttaacattaa cgcctaataa acacagatta 300  
 gaagaatacg ttaaatatca acaagaggat tacgaatctg atattttaga aaaacgtgaa 360  
 tctagacgt atcgtgaaag agaagaataa ttgaatgaaa tatctactat aatggtgggt 420  
 ttaaagctat caacaatttt gttgatagct attttatgt ttcaaacata taaatattat 480  
 ttacttgcga ttgataacca ttctcaatta ataaaaataa cttatagtagc aatgcgtta 540  
 taataagtt tacttatact acctgattaa aaatgcgaaa tgaaaaatga cccctttata 600  
 tacctataca gttgtgttcg aaaacatata ataatacaat ttaactaagg catataaata 660  
 tatagaaatt caagggggat atcaa atg gct tct aat ttt aaa gaa aca gcg 712  
 Met Ala Ser Asn Phe Lys Glu Thr Ala  
 1 5  
 aag aaa caa ttt gat tta aat ggc caa tca tac acg tac tat gat tta 760  
 Lys Lys Gln Phe Asp Leu Asn Gly Gln Ser Tyr Thr Tyr Tyr Asp Leu  
 15 20  
 aaa tca tta gaa gaa caa ggt tta act aaa att tca aag tta cct tat 808  
 Lys Ser Leu Glu Glu Gln Gly Leu Thr Lys Ile Ser Lys Leu Pro Tyr  
 30 35 40  
 tca atc cgt gta tta cta gaa tca gtg tta cgt cag gaa gat gat ttt 856  
 Ser Ile Arg Val Leu Leu Glu Ser Val Leu Arg Gln Glu Asp Asp Phe  
 45 50 55  
 gta att act gat gat cac att aaa caa tta gca gaa ttt ggc aaa aaa 904  
 Val Ile Thr Asp Asp His Ile Lys Gln Leu Ala Glu Phe Gly Lys Lys  
 60 65 70  
 ggt aac gaa ggt gaa gta cct ttc aaa cca tct cga gtt att tta caa 952  
 Gly Asn Glu Gly Glu Val Pro Phe Lys Pro Ser Arg Val Ile Leu Gln  
 75 80 85  
 gac ttc act ggt gta cca gca gta gtt gac tta gcg tct tta cgt aaa 1000  
 Asp Phe Thr Gly Val Pro Ala Val Val Asp Leu Ala Ser Leu Arg Lys  
 90 95 100 105  
 gca atg aat gat gtt ggt ggg gat att aat aaa att aac cct gaa gta 1048  
 Ala Met Asn Asp Val Gly Gly Asp Ile Asn Lys Ile Asn Pro Glu Val  
 110 115 120  
 cca gtt gac tta gtt att gac cac tct gta caa gta gat agt tat gct 1096  
 Pro Val Asp Leu Val Ile Asp His Ser Val Gln Val Asp Ser Tyr Ala  
 125 130 135  
 aat cca gat gca tta caa cgt aac atg aaa tta gaa ttt gaa cgt aac 1144  
 Asn Pro Asp Ala Leu Gln Arg Asn Met Lys Leu Glu Phe Glu Arg Asn

140	145	150	
tat gaa cgt tac caa ttc tta aac tgg gca aca aaa gca ttt gat aac			1192
Tyr Glu Arg Tyr Gln Phe Leu Asn Trp Ala Thr Lys Ala Phe Asp Asn			
155 160 165			
tat aat gca gta cca cct gct aca ggt att gtc cac caa gta aac tta			1240
Tyr Asn Ala Val Pro Pro Ala Thr Gly Ile Val His Gln Val Asn Leu			
170 175 180 185			
gaa tac tta gcg aat gtt gta cat gtt cgt gac gtt gac gga gaa caa			1288
Glu Tyr Leu Ala Asn Val Val His Val Arg Asp Val Asp Gly Glu Gln			
190 195 200			
act gct ttc cca gat aca tta gtt ggt act gac tca cat act aca atg			1336
Thr Ala Phe Pro Asp Thr Leu Val Gly Thr Asp Ser His Thr Thr Met			
205 210 215			
att aac ggt att ggt gta tta ggt tgg ggt gtc ggc ggt atc gaa gct			1384
Ile Asn Gly Ile Gly Val Leu Gly Trp Gly Val Gly Gly Ile Glu Ala			
220 225 230			
gaa gca ggt atg tta gga caa cca tca tac ttc cca att cca gaa gtt			1432
Glu Ala Gly Met Leu Gly Gln Pro Ser Tyr Phe Pro Ile Pro Glu Val			
235 240 245			
att ggt gtt aaa tta agt aat gaa tta cca caa ggt tca aca gca act			1480
Ile Gly Val Lys Leu Ser Asn Glu Leu Pro Gln Gly Ser Thr Ala Thr			
250 255 260 265			
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Asp Leu Ala Leu Arg Val Thr Glu Glu Leu Arg Lys Arg Gly Val Val			
270 275 280			
ggt aaa ttc gtt gag ttc ttt ggt cct ggt gta aca aac tta cca tta			1576
Gly Lys Phe Val Glu Phe Phe Gly Pro Gly Val Thr Asn Leu Pro Leu			
285 290 295			
gct gac cgt gca aca att gcg aac atg gcg cct gaa tat ggt gca act			1624
Ala Asp Arg Ala Thr Ile Ala Asn Met Ala Pro Glu Tyr Gly Ala Thr			
300 305 310			
tgt ggt ttc ttc cca gtt gat gaa gaa tca ctt aaa tac atg aaa tta			1672
Cys Gly Phe Phe Pro Val Asp Glu Glu Ser Leu Lys Tyr Met Lys Leu			
315 320 325			
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Thr Gly Arg Lys Asp Asp His Ile Ala Leu Val Lys Glu Tyr Leu Gln			
330 335 340 345			
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Gln Asn Asn Met Phe Phe Gln Val Glu Asn Glu Asp Pro Glu Tyr Thr			
350 355 360			
gaa gtg att gat tta gat tta tct aca gtt caa gct tct tta tca ggt			1816
Glu Val Ile Asp Leu Asp Leu Ser Thr Val Gln Ala Ser Leu Ser Gly			
365 370 375			
cca aaa cgt cca caa gat tta atc ttc tta agt gac atg aaa act gaa			1864
Pro Lys Arg Pro Gln Asp Leu Ile Phe Leu Ser Asp Met Lys Thr Glu			
380 385 390			
ttc gaa aaa tca gtt aca gca cca gct ggt aac caa ggt cac ggt tta			1912
Phe Glu Lys Ser Val Thr Ala Pro Ala Gly Asn Gln Gly His Gly Leu			
395 400 405			
gat gaa agt gaa ttt gat aag aaa gca gaa atc aaa ttt aat gat ggt			1960
Asp Glu Ser Glu Phe Asp Lys Lys Ala Glu Ile Lys Phe Asn Asp Gly			

410	415	420	425	
aga act tca act atg aag act ggt gat gtt gcg att gca gcg att aca				2008
Arg Thr Ser Thr Met Lys Thr Gly Asp Val Ala Ile Ala Ala Ile Thr				
430	435	440		
tca tgt aca aat aca tct aac cct tac gtt atg tta ggt gca ggt tta				2056
Ser Cys Thr Asn Thr Ser Asn Pro Tyr Val Met Leu Gly Ala Gly Leu				
445	450	455		
gta gct aaa aaa gca att gaa aaa ggc tta aaa gta cct gat tat gta				2104
Val Ala Lys Lys Ala Ile Glu Lys Gly Leu Lys Val Pro Asp Tyr Val				
460	465	470		
aaa act tca tta gca cca ggt tca aaa gtt gtt act gga tat tta aga				2152
Lys Thr Ser Leu Ala Pro Gly Ser Lys Val Val Thr Gly Tyr Leu Arg				
475	480	485		
gat tca ggt tta caa gaa tat ctt gat gac tta ggt ttc aac tta gtt				2200
Asp Ser Gly Leu Gln Glu Tyr Leu Asp Asp Leu Gly Phe Asn Leu Val				
490	495	500	505	
ggt tat ggt tgt aca act tgt atc ggt aac tca ggt cca tta tta cct				2248
Gly Tyr Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Leu Pro				
510	515	520		
gaa att gaa aaa gca gta gct gac gaa gat tta tta gta act tct gta				2296
Glu Ile Glu Lys Ala Val Ala Asp Glu Asp Leu Leu Val Thr Ser Val				
525	530	535		
ctt tct ggt aac cgt aac ttt gaa ggt cgt atc cat ccg tta gtt aaa				2344
Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile His Pro Leu Val Lys				
540	545	550		
gct aac tac tta gct tca cca caa tta gtt gta gct tat gca tta gct				2392
Ala Asn Tyr Leu Ala Ser Pro Gln Leu Val Val Ala Tyr Ala Leu Ala				
555	560	565		
gga acg gtt gat atc gat tta cac aat gaa cct atc ggt aaa ggt aaa				2440
Gly Thr Val Asp Ile Asp Leu His Asn Glu Pro Ile Gly Lys Gly Lys				
570	575	580	585	
gat ggc gaa gat gta tac ctt aaa gat atc tgg cca agt atc aaa gaa				2488
Asp Gly Glu Asp Val Tyr Leu Lys Asp Ile Trp Pro Ser Ile Lys Glu				
590	595	600		
gtt gca gac act gtt gat agt gtc gta acg cca gaa tta ttc tta gaa				2536
Val Ala Asp Thr Val Asp Ser Val Val Thr Pro Glu Leu Phe Leu Glu				
605	610	615		
gaa tat gca aat gta tac gaa aat aat gaa atg tgg aat gaa atc gac				2584
Glu Tyr Ala Asn Val Tyr Glu Asn Asn Glu Met Trp Asn Glu Ile Asp				
620	625	630		
gtt act gac gca cca tta tat gat ttc gat cca aat tca act tat att				2632
Val Thr Asp Ala Pro Leu Tyr Asp Phe Asp Pro Asn Ser Thr Tyr Ile				
635	640	645		
caa aat cca tca ttc ttc caa ggt tta tct aaa gaa cca gga act att				2680
Gln Asn Pro Ser Phe Phe Gln Gly Leu Ser Lys Glu Pro Gly Thr Ile				
650	655	660	665	
gaa cca tta aaa gat tta cgt att atg ggt aaa ttt ggt gat tca gtt				2728
Glu Pro Leu Lys Asp Leu Arg Ile Met Gly Lys Phe Gly Asp Ser Val				
670	675	680		
aca act gac cac att tct cca gca ggt gcg atc ggt aaa gat aca cca				2776
Thr Thr Asp His Ile Ser Pro Ala Gly Ala Ile Gly Lys Asp Thr Pro				

685	690	695	
gca ggt aaa tat tta tta gac cat gat gtt cca att aga gaa ttt aac			2824
Ala Gly Lys Tyr Leu Leu Asp His Asp Val Pro Ile Arg Glu Phe Asn			
700	705	710	
tct tat ggt tca aga cgt ggt aac cat gaa gta atg gta cgt ggt act			2872
Ser Tyr Gly Ser Arg Arg Gly Asn His Glu Val Met Val Arg Gly Thr			
715	720	725	
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Phe Ala Asn Ile Arg Ile Lys Asn Gln Leu Ala Pro Gly Thr Glu Gly			
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gga ttt aca aca tat tgg cct aca gaa gaa atc atg cct atc tat gat			2968
Gly Phe Thr Thr Tyr Trp Pro Thr Glu Glu Ile Met Pro Ile Tyr Asp			
750	755	760	
gca gct atg aga tac aaa gaa aat ggt act ggt tta gct gtt tta gct			3016
Ala Ala Met Arg Tyr Lys Glu Asn Gly Thr Gly Leu Ala Val Leu Ala			
765	770	775	
ggt aat gat tac ggt atg ggt tca tct cgt gac tgg gca gct aaa ggt			3064
Gly Asn Asp Tyr Gly Met Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly			
780	785	790	
act aac tta tta ggt gtt aaa act gtt att gca caa agt tat gaa cgt			3112
Thr Asn Leu Leu Gly Val Lys Thr Val Ile Ala Gln Ser Tyr Glu Arg			
795	800	805	
atc cat cgt tca aac tta gta atg atg ggt gta tta cca tta caa ttt			3160
Ile His Arg Ser Asn Leu Val Met Met Gly Val Leu Pro Leu Gln Phe			
810	815	820	825
aaa caa ggt gag tca gct gat tct cta ggt tta gaa ggt aaa gaa gaa			3208
Lys Gln Gly Glu Ser Ala Asp Ser Leu Gly Leu Glu Gly Lys Glu Glu			
830	835	840	
att tct gta gat atc gat gaa aat gtt aaa cca cat gat tta gta act			3256
Ile Ser Val Asp Ile Asp Glu Asn Val Lys Pro His Asp Leu Val Thr			
845	850	855	
gtt cat gct aaa aaa gaa aac gga gaa gtt gtt gat ttt gaa gca atg			3304
Val His Ala Lys Lys Glu Asn Gly Glu Val Val Asp Phe Glu Ala Met			
860	865	870	
gtt cgt ttc gat tca tta gta gaa tta gat tat tat cgt cat ggt ggt			3352
Val Arg Phe Asp Ser Leu Val Glu Leu Asp Tyr Tyr Arg His Gly Gly			
875	880	885	
atc tta caa atg gta tta aga aac aaa tta gct caa taatcacaat			3398
Ile Leu Gln Met Val Leu Arg Asn Lys Leu Ala Gln			
890	895	900	
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<212> PRT

<213> Corynebacterium thermoaminogenes

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Leu	Thr	Lys	Ile	Ser	Lys	Leu	Pro	Tyr	Ser	Ile	Arg	Val	Leu	Leu	Glu
				35			40				45				
Ser	Val	Leu	Arg	Gln	Glu	Asp	Asp	Phe	Val	Ile	Thr	Asp	Asp	His	Ile
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Lys	Gln	Leu	Ala	Glu	Phe	Gly	Lys	Gly	Asn	Glu	Gly	Glu	Val	Pro	
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Phe	Lys	Pro	Ser	Arg	Val	Ile	Leu	Gln	Asp	Phe	Thr	Gly	Val	Pro	Ala
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Val	Val	Asp	Leu	Ala	Ser	Leu	Arg	Lys	Ala	Met	Asn	Asp	Val	Gly	Gly
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Asp	Ile	Asn	Lys	Ile	Asn	Pro	Glu	Val	Pro	Val	Asp	Leu	Val	Ile	Asp
				115			120				125				
His	Ser	Val	Gln	Val	Asp	Ser	Tyr	Ala	Asn	Pro	Asp	Ala	Leu	Gln	Arg
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Asn	Met	Lys	Leu	Glu	Phe	Glu	Arg	Asn	Tyr	Glu	Arg	Tyr	Gln	Phe	Leu
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Thr	Gly	Ile	Val	His	Gln	Val	Asn	Leu	Glu	Tyr	Leu	Ala	Asn	Val	Val
				180			185				190				
His	Val	Arg	Asp	Val	Asp	Gly	Glu	Gln	Thr	Ala	Phe	Pro	Asp	Thr	Leu
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Pro	Ser	Tyr	Phe	Pro	Ile	Pro	Glu	Val	Ile	Gly	Val	Lys	Leu	Ser	Asn
				245			250				255				
Glu	Leu	Pro	Gln	Gly	Ser	Thr	Ala	Thr	Asp	Leu	Ala	Leu	Arg	Val	Thr
				260			265				270				
Glu	Glu	Leu	Arg	Lys	Arg	Gly	Val	Val	Gly	Lys	Phe	Val	Glu	Phe	Phe
				275			280				285				
Gly	Pro	Gly	Val	Thr	Asn	Leu	Pro	Leu	Ala	Asp	Arg	Ala	Thr	Ile	Ala
				290			295				300				
Asn	Met	Ala	Pro	Glu	Tyr	Gly	Ala	Thr	Cys	Gly	Phe	Phe	Pro	Val	Asp
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Glu	Glu	Ser	Leu	Lys	Tyr	Met	Lys	Leu	Thr	Gly	Arg	Lys	Asp	Asp	His
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Ile	Ala	Leu	Val	Lys	Glu	Tyr	Leu	Gln	Gln	Asn	Asn	Met	Phe	Phe	Gln
				340			345				350				
Val	Glu	Asn	Glu	Asp	Pro	Glu	Tyr	Thr	Glu	Val	Ile	Asp	Leu	Asp	Leu
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 Pro Ala Gly Asn Gln Gly His Gly Leu Asp Glu Ser Glu Phe Asp Lys  
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 Lys Ala Glu Ile Lys Phe Asn Asp Gly Arg Thr Ser Thr Met Lys Thr  
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 Gly Asp Val Ala Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser Asn  
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 Pro Tyr Val Met Leu Gly Ala Gly Leu Val Ala Lys Lys Ala Ile Glu  
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 Lys Gly Leu Lys Val Pro Asp Tyr Val Lys Thr Ser Leu Ala Pro Gly  
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 Ser Lys Val Val Thr Gly Tyr Leu Arg Asp Ser Gly Leu Gln Glu Tyr  
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 Ile Gly Asn Ser Gly Pro Leu Leu Pro Glu Ile Glu Lys Ala Val Ala  
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 Asp Glu Asp Leu Leu Val Thr Ser Val Leu Ser Gly Asn Arg Asn Phe  
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 Glu Gly Arg Ile His Pro Leu Val Lys Ala Asn Tyr Leu Ala Ser Pro  
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 Gln Leu Val Val Ala Tyr Ala Leu Ala Gly Thr Val Asp Ile Asp Leu  
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 His Asn Glu Pro Ile Gly Lys Gly Lys Asp Gly Glu Asp Val Tyr Leu  
 580 585 590  
 Lys Asp Ile Trp Pro Ser Ile Lys Glu Val Ala Asp Thr Val Asp Ser  
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 Val Val Thr Pro Glu Leu Phe Leu Glu Glu Tyr Ala Asn Val Tyr Glu  
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 Asp Phe Asp Pro Asn Ser Thr Tyr Ile Gln Asn Pro Ser Phe Phe Gln  
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 Gly Leu Ser Lys Glu Pro Gly Thr Ile Glu Pro Leu Lys Asp Leu Arg  
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 725 730 735  
 Asn Gln Leu Ala Pro Gly Thr Glu Gly Gly Phe Thr Thr Tyr Trp Pro  
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 Thr Glu Glu Ile Met Pro Ile Tyr Asp Ala Ala Met Arg Tyr Lys Glu  
 755 760 765  
 Asn Gly Thr Gly Leu Ala Val Leu Ala Gly Asn Asp Tyr Gly Met Gly

770	775	780
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785	790	795
Thr Val Ile Ala Gln Ser Tyr Glu Arg Ile His Arg Ser Asn Leu Val		815
805	810	
Met Met Gly Val Leu Pro Leu Gln Phe Lys Gln Gly Glu Ser Ala Asp		830
820	825	
Ser Leu Gly Leu Glu Gly Lys Glu Glu Ile Ser Val Asp Ile Asp Glu		845
835	840	
Asn Val Lys Pro His Asp Leu Val Thr Val His Ala Lys Lys Glu Asn		860
850	855	
Gly Glu Val Val Asp Phe Glu Ala Met Val Arg Phe Asp Ser Leu Val		880
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Glu Leu Asp Tyr Tyr Arg His Gly Gly Ile Leu Gln Met Val Leu Arg		895
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Asn Lys Leu Ala Gln		
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 <213> Corynebacterium thermoaminogenes

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tgatatcgct tccctgaggg tccgcaggcg tgcctcaccc tgtattctg atagttgaac	354
aaaagagccc acataacaag gagactc atg gct aag atc atc tgg acc cgc acc	
Met Ala Lys Ile Ile Trp Thr Arg Thr	
1 5	402
gac gaa gca ccg ctg ctc gcg acc tac tcg ctg aag ccg gtc gtc gag	
Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys Pro Val Val Glu	
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gct ttc gcc gcc acc gcg ggc atc gag gtg gag acc cgc gat atc tct	
Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr Arg Asp Ile Ser	
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ctc gcc ggt cgc atc ctc gca cag ttc gcg gac cag ctc ccc gag gag	
Leu Ala Gly Arg Ile Leu Ala Gln Phe Ala Asp Gln Leu Pro Glu Glu	
45 50 55	546
cag aag gtc tcc gac gcc ctc gag ctc ggc gaa ctg gct aag acc	
Gln Lys Val Ser Asp Ala Leu Ala Glu Leu Gly Glu Leu Ala Lys Thr	
60 65 70	594
ccc gaa gcc aac atc atc aag ctt ccc aac atc tcc gca tcc gta ccg	
Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser Ala Ser Val Pro	
75 80 85	

cag ctc aag gct gcc gta aag gaa ctg cag gaa cag ggc tac gac ctg	642
Gln Leu Lys Ala Ala Val Lys Glu Leu Gln Glu Gln Gly Tyr Asp Leu	
95 100 105	
ccc gag tac gag gat gcc aag gac cgc tac gcc gct gtc atc ggc tcc	690
Pro Glu Tyr Glu Asp Ala Lys Asp Arg Tyr Ala Ala Val Ile Gly Ser	
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aac gtc aac ccg gtc ctg cgc gag ggc aac tcc gac cgc cgc gca ccg	738
Asn Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro	
125 130 135	
gtg gcc gtg aag aac ttc gtg aag aag ttc ccc cac cgc atg ggc gag	786
Val Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu	
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tgg tcc gcc gac tcc aag acc aac gtt gcc acc atg ggt gcc gac gac	834
Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Gly Ala Asp Asp	
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ttc cgc agc aat gag aag tcc gtg atc atg gac gag gcc gac acc gtg	882
Phe Arg Ser Asn Glu Lys Ser Val Ile Met Asp Glu Ala Asp Thr Val	
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gtg atc aag cat gtc gcc gac ggc acc gag acc gtg ctc aag gac	930
Val Ile Lys His Val Ala Ala Asp Gly Thr Glu Thr Val Leu Lys Asp	
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agc ctc ccc ctg ctc aag ggt gag gtc atc gac ggc acc ttc atc tcc	978
Ser Leu Pro Leu Leu Lys Gly Glu Val Ile Asp Gly Thr Phe Ile Ser	
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Ala Lys Ala Leu Asp Ala Phe Leu Leu Asp Gln Val Lys Arg Ala Lys	
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gag gag ggc atc ctc ttc tcc gcc cac atg aag gcc acc atg atg aag	1074
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Val Ser Asp Pro Ile Ile Phe Gly His Ile Val Arg Ala Tyr Phe Ala	
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Asp Val Tyr Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly Leu Asn	
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Gly Glu Asn Gly Leu Ala Ala Ile Tyr Ala Gly Leu Asp Lys Leu Asp	
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Asn Gly Ala Glu Ile Lys Ala Ala Phe Asp Lys Gly Leu Glu Glu Gly	
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Pro Asp Leu Ala Met Val Asn Ser Ala Lys Gly Ile Thr Asn Leu His	
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Val Pro Ser Asp Val Ile Ile Asp Ala Ser Met Pro Ala Met Ile Arg	
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Thr Ser Gly Lys Met Trp Asn Lys Asp Asp Gln Thr Gln Asp Ala Leu	
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Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr Gly Ser	
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His Asp Lys Thr Phe Arg Ile Glu Ala Asp Gly Lys Val Gln Val Val	
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Trp Leu Asp Pro Ala Arg Ala His Asp Arg Asn Leu Thr Thr Leu Val	
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Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile Gln Ile	
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Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe	
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Arg His Glu Leu Asn Thr Arg Asn Asn Thr Lys Ala Gly Val Leu Ala	
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 Glu Gly Asn Ser Asp Arg Arg Ala Pro Val Ala Val Lys Asn Phe Val

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 580 585 590  
 Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn Thr Arg  
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 Pro Val Ala Glu Ala Leu Asn Asn Gln Ala Ala Asp Ile Asp Ala Ala  
 675 680 685  
 Leu Ile Gly Glu Gln Gly Lys Pro Val Asp Leu Gly Gly Tyr Tyr Ala  
 690 695 700  
 Pro Ser Asp Glu Lys Thr Ser Ala Ile Met Arg Pro Val Ala Ala Phe  
 705 710 715 720  
 Asn Glu Ile Ile Asp Ser Leu Lys Lys  
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 cctaggctct gccgatgcta aaagtcagct gacccttgg ggcgccttcat ttgaaactgc 180  
 gaccaagctc atgaatgcgc gaaagcattt ccattataag ggttaagctgt aagaatagt 240  
 ggagaaaatg ttcagtcgtg ttcttaactca cttgagaaat tccatttttc tgggcttctc 300  
 tcaaataatgt taagtggccc gtatgctgga tttctagaat atttagaagc ggcacaactc 360  
 atgattatgt attgtataag cctcaaagac cgaatagatt actaacattt aagtggacca 420  
 gagcgtaga agctttgttag agtgctcatt ccttgcgtac ggcaagggtt tcctaccatg 480  
 agatagatcg gcagatagtt ggtttgtaaa aattttaag gacggccgc aatgtcaatt 540  
 cttgaacaga tcatcttctt catcaacacc atcttgggtt atggtctgca cgctggttct 600  
 tccgcttcca gcaaccttc tcacacgatc ggcctgtct aggcctaatt gtaataagg 660  
 ctgtgttaaca gtcgccccgct tgattgtgtc tttttaggct cccgcgcggg cgattttcgg 720  
 ttttcatctt ttttaatgt agtttggaaag atcaagtgcc cccggatgca cgacaatgt 780  
 atgccgaaca cgtattgttg aaatc gtg act gaa cat tat gac gta gta gta  
 Val Thr Glu His Tyr Asp Val Val Val 832

ctc	gga	gct	ggc	ccc	ggt	ggc	tat	gtc	tcc	gcc	atc	cgc	gcc	gct	cag	880
Leu	Gly	Ala	Gly	Pro	Gly	Gly	Tyr	Val	Ser	Ala	Ile	Arg	Ala	Ala	Gln	
10							15				20				25	
ctc	ggt	aag	aaa	gtt	gct	gtt	atc	gag	aag	cag	tac	tgg	gga	ggt	gtc	928
Leu	Gly	Lys	Lys	Val	Ala	Val	Ile	Glu	Lys	Gln	Tyr	Trp	Gly	Gly	Val	
							30			35			40			
tgc	ctg	aat	gtg	ggt	tgt	atc	cca	tct	aag	gct	ttg	atc	aag	aac	gct	976
Cys	Leu	Asn	Val	Gly	Cys	Ile	Pro	Ser	Lys	Ala	Leu	Ile	Lys	Asn	Ala	
							45			50			55			
gag	atc	gcc	cac	atc	tcc	aac	cat	gag	aag	aag	acc	ttc	ggc	atc	aac	1024
Glu	Ile	Ala	His	Ile	Phe	Asn	His	Glu	Lys	Lys	Thr	Phe	Gly	Ile	Asn	
							60			65			70			
ggc	gag	gtc	acc	tcc	aac	tac	gag	gat	gcc	cac	aag	cgt	tcc	cgt	ggt	1072
Gly	Glu	Val	Thr	Phe	Asn	Tyr	Glu	Asp	Ala	His	Lys	Arg	Ser	Arg	Gly	
							75			80			85			
gtc	tcc	gac	aag	atc	gtc	ggc	ggt	gtt	cac	tac	ttg	atg	aag	aag	aac	1120
Val	Ser	Asp	Lys	Ile	Val	Gly	Gly	Val	His	Tyr	Leu	Met	Lys	Lys	Asn	
							90			95			100			105
aag	atc	acc	gag	atc	gac	ggt	tcc	ggc	acc	ttc	aag	gat	gcc	aag	acc	1168
Lys	Ile	Thr	Glu	Ile	Asp	Gly	Phe	Gly	Thr	Phe	Lys	Asp	Ala	Lys	Thr	
							110			115			120			
atc	gag	gtg	acc	gat	ggt	aag	gat	gcc	ggc	aag	acc	gtc	acc	tcc	gat	1216
Ile	Glu	Val	Thr	Asp	Gly	Lys	Asp	Ala	Gly	Lys	Thr	Val	Thr	Phe	Asp	
							125			130			135			
gac	tgc	atc	atc	gcc	acc	ggt	tcc	gtg	gtc	aac	tcc	ctc	cgt	ggt	gtt	1264
Asp	Cys	Ile	Ile	Ala	Thr	Gly	Ser	Val	Val	Asn	Ser	Leu	Arg	Gly	Val	
							140			145			150			
gag	tcc	tcc	gag	aac	gtg	gtc	tcc	tac	gag	gag	cag	atc	ctc	aac	ccg	1312
Glu	Phe	Ser	Glu	Asn	Val	Val	Ser	Tyr	Glu	Glu	Gln	Ile	Leu	Asn	Pro	
							155			160			165			
gtg	gct	cct	aag	aag	atg	gtc	atc	gtc	ggt	ggc	ggc	gcc	atc	ggt	atg	1360
Val	Ala	Pro	Lys	Lys	Met	Val	Ile	Val	Gly	Gly	Gly	Ala	Ile	Gly	Met	
							170			175			180			185
gaa	tcc	gcc	tac	gtt	ctg	ggc	aac	tac	ggt	gtg	gac	gta	acc	ctc	atc	1408
Glu	Phe	Ala	Tyr	Val	Leu	Gly	Asn	Tyr	Gly	Val	Asp	Val	Thr	Leu	Ile	
							190			195			200			
gag	tcc	atg	gac	cgc	gtt	ctg	ccg	aac	gag	gat	cca	gag	gtg	tcc	aag	1456
Glu	Phe	Met	Asp	Arg	Val	Leu	Pro	Asn	Glu	Asp	Pro	Glu	Val	Ser	Lys	
							205			210			215			
gtt	atc	gcc	aag	gcc	tac	aag	aag	atg	ggc	atc	aag	ctc	ctc	ccg	ggc	1504
Val	Ile	Ala	Lys	Ala	Tyr	Lys	Lys	Met	Gly	Ile	Lys	Leu	Leu	Pro	Gly	
							220			225			230			
cac	gca	acc	acc	gct	cgc	gac	aat	ggc	gat	tcc	gtt	gag	gtc	gat		1552
His	Ala	Thr	Thr	Ala	Val	Arg	Asp	Asn	Gly	Asp	Ser	Val	Glu	Val	Asp	
							235			240			245			
tac	cag	aag	aag	ggc	tcg	gac	aag	acc	gag	acc	atc	acc	gtc	gac	cgt	1600
Tyr	Gln	Lys	Lys	Gly	Ser	Asp	Lys	Thr	Glu	Thr	Ile	Thr	Val	Asp	Arg	
							250			255			260			265
gtt	ctt	atc	tcc	gtc	ggc	tcc	cgc	cca	cgc	gtc	gag	ggc	tcc	ggc	ctg	1648
Val	Leu	Ile	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	
							270			275			280			

gag aac acc ggc gtc aag ctc acc gaa cgc ggt gcc atc gac att gat	1696
Glu Asn Thr Gly Val Lys Leu Thr Glu Arg Gly Ala Ile Asp Ile Asp	
285 290 295	
gag cat atg cgc acc aac gtc gac ggc atc tac gcc atc ggt gac gtc	1744
Glu His Met Arg Thr Asn Val Asp Gly Ile Tyr Ala Ile Gly Asp Val	
300 305 310	
acc gcc aag ctg cag ctg gca cac gtc gcc gag gca cag ggc att gtc	1792
Thr Ala Lys Leu Gln Leu Ala His Val Ala Glu Ala Gln Gly Ile Val	
315 320 325	
gcc gcc gag aca ctc gcc ggc gca gaa acc cag acc ctg ggc gac tac	1840
Ala Ala Glu Thr Leu Ala Gly Ala Glu Thr Gln Thr Leu Gly Asp Tyr	
330 335 340 345	
atg atg atg ccg cgt gcc acc ttc tgc aac cca cag gtt gcc tcc ttc	1888
Met Met Met Pro Arg Ala Thr Phe Cys Asn Pro Gln Val Ala Ser Phe	
350 355 360	
ggt tac acc gag gag cag gcc aag gag aag tgg ccg gat cga gag atc	1936
Gly Tyr Thr Glu Glu Gln Ala Lys Glu Lys Trp Pro Asp Arg Glu Ile	
365 370 375	
aag gtg tcc tcc ttc ccg ttc tcc gcg aac ggc aag gcc gtc ggc ctg	1984
Lys Val Ser Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu	
380 385 390	
gct gag acc gat ggt ttc gcc aag atc gtc gcc gac gct gag ttc ggt	2032
Ala Glu Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly	
395 400 405	
gaa ctg ctg ggt ggc cac att gtc ggt gcc aac gcc tcc gag ctg ctc	2080
Glu Leu Leu Gly Gly His Ile Val Gly Ala Asn Ala Ser Glu Leu Leu	
410 415 420 425	
aac gag ctg gtg ctg gcc cag aac tgg gat ctc acc acc gag gag atc	2128
Asn Glu Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile	
430 435 440	
agc cgc agc gtc cac atc cac ccg acc ctg tcg gag gct gtc aag gaa	2176
Ser Arg Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu	
445 450 455	
gct gcc cac ggc gtc aac ggc cac atg atc aac ttc taaatcccg	2222
Ala Ala His Gly Val Asn Gly His Met Ile Asn Phe	
460 465	
cagacaaatg caaatccct caccgatggc atatcggtga ggggattttc tcatgcacgt	2282
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Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val	
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Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile	
35 40 45	

Pro Ser Lys Ala Leu Ile Lys Asn Ala Glu Ile Ala His Ile Phe Asn  
     50                    55                    60  
 His Glu Lys Lys Thr Phe Gly Ile Asn Gly Glu Val Thr Phe Asn Tyr  
     65                    70                    75                    80  
 Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly  
     85                    90                    95  
 Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Thr Glu Ile Asp Gly  
     100                    105                    110  
 Phe Gly Thr Phe Lys Asp Ala Lys Thr Ile Glu Val Thr Asp Gly Lys  
     115                    120                    125  
 Asp Ala Gly Lys Thr Val Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly  
     130                    135                    140  
 Ser Val Val Asn Ser Leu Arg Gly Val Glu Phe Ser Glu Asn Val Val  
     145                    150                    155                    160  
 Ser Tyr Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val  
     165                    170                    175  
 Ile Val Gly Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly  
     180                    185                    190  
 Asn Tyr Gly Val Asp Val Thr Leu Ile Glu Phe Met Asp Arg Val Leu  
     195                    200                    205  
 Pro Asn Glu Asp Pro Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys  
     210                    215                    220  
 Lys Met Gly Ile Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg  
     225                    230                    235                    240  
 Asp Asn Gly Asp Ser Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp  
     245                    250                    255  
 Lys Thr Glu Thr Ile Thr Val Asp Arg Val Leu Ile Ser Val Gly Phe  
     260                    265                    270  
 Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu  
     275                    280                    285  
 Thr Glu Arg Gly Ala Ile Asp Ile Asp Glu His Met Arg Thr Asn Val  
     290                    295                    300  
 Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala  
     305                    310                    315                    320  
 His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Leu Ala Gly  
     325                    330                    335  
 Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr  
     340                    345                    350  
 Phe Cys Asn Pro Gln Val Ala Ser Phe Gly Tyr Thr Glu Glu Gln Ala  
     355                    360                    365  
 Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ser Ser Phe Pro Phe  
     370                    375                    380  
 Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala  
     385                    390                    395                    400  
 Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Gly His Ile  
     405                    410                    415  
 Val Gly Ala Asn Ala Ser Glu Leu Leu Asn Glu Leu Val Leu Ala Gln  
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 Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His  
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 Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Val Asn Gly

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His																
Met																
Ile																
Asn																
Phe																
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aaagacttgt	taccaaaagg	tgctaatact	ggggtgctag	gtccccgcga	ccggaaccag	180										
cgttacagtg	gataaaataa	agccattta	gaaccctcaa	caagcaagga	aaagaggcga	240										
gtacctgcc	gtg	agc	gct	agt	act	ttc	ggc	cag	aac	gcg	tgg	ctg	gtg	291		
	Val	Ser	Ser	Ala	Ser	Thr	Phe	Gly	Gln	Asn	Ala	Trp	Leu	Val		
	1		5			10										
gat	gag	atg	ttc	cag	cag	ttc	aag	aag	gac	ccc	cag	tcc	gtg	gac	aag	339
Asp	Glu	Met	Phe	Gln	Gln	Phe	Lys	Lys	Asp	Pro	Gln	Ser	Val	Asp	Lys	
		15			20					25					30	
gaa	tgg	aga	gag	ctc	ttc	gag	tct	cag	ggg	ggt	ccc	cag	gct	gaa	aag	387
Glu	Trp	Arg	Glu	Leu	Phe	Ser	Gln	Gly	Gly	Gly	Pro	Gln	Ala	Glu	Lys	
				35					40					45		
gct	acc	ccc	gcc	acc	ccc	gaa	gcc	aag	aag	gca	gct	tcg	tcg	cag	tcc	435
Ala	Thr	Pro	Ala	Thr	Pro	Glu	Ala	Lys	Lys	Ala	Ala	Ser	Ser	Gln	Ser	
				50					55					60		
tca	act	tcc	gga	cag	tcc	acc	gcc	aag	gct	gcc	cct	gcc	gcc	aag	acc	483
Ser	Thr	Ser	Gly	Gln	Ser	Thr	Ala	Lys	Ala	Ala	Ala	Pro	Ala	Ala	Lys	
		65			70					75						
gca	ccg	gcc	tct	gcg	cca	gcc	aag	gct	gcc	cct	gtt	aag	caa	aac	cag	531
Ala	Pro	Ala	Ser	Ala	Pro	Ala	Lys	Ala	Ala	Pro	Val	Lys	Gln	Asn	Gln	
		80			85					90						
gcg	tcc	aag	cct	gcc	aag	aag	gcc	aag	gag	tcc	ccc	ctg	tcc	aag	cca	579
Ala	Ser	Lys	Pro	Ala	Lys	Lys	Ala	Lys	Glu	Ser	Pro	Leu	Ser	Lys	Pro	
		95			100					105					110	
gct	gcc	atg	cct	gag	ccg	gga	acc	acc	cca	ctc	agg	ggc	atc	ttc	aag	627
Ala	Ala	Met	Pro	Glu	Pro	Gly	Thr	Thr	Pro	Leu	Arg	Gly	Ile	Phe	Lys	
		115							120					125		
tcc	atc	gcc	aag	aac	atg	gac	ctc	tcc	ctc	gag	gtg	ccc	acc	gcc	acc	675
Ser	Ile	Ala	Lys	Asn	Met	Asp	Leu	Ser	Leu	Glu	Val	Pro	Thr	Ala	Thr	
		130			135					140						
tcc	gtc	cgc	gac	atg	ccc	gcg	cgc	ctc	atg	ttc	gag	aac	cgc	gcc	atg	723
Ser	Val	Arg	Asp	Met	Pro	Ala	Arg	Leu	Met	Phe	Glu	Asn	Arg	Ala	Met	
		145			150					155						
gtc	aac	gac	cag	ctc	aag	cgc	acc	cgt	ggc	ggc	aag	atc	tcc	ttc	acc	771
Val	Asn	Asp	Gln	Leu	Lys	Arg	Thr	Arg	Gly	Gly	Lys	Ile	Ser	Phe	Thr	
		160			165					170						

175	180	185	190	819
atg aac aac tcc tat gac atc gtc gac ggc aag ccg tcc ctg gtc gtc	867			
Met Asn Asn Ser Tyr Asp Ile Val Asp Gly Lys Pro Ser Leu Val Val				
195	200	205		
ccg gag cac atc aac ctc ggc ctg gcc atc gac ctc ccc cag aag gac	915			
Pro Glu His Ile Asn Leu Gly Leu Ala Ile Asp Leu Pro Gln Lys Asp				
210	215	220		
ggc tcc cgt gcc ctc gtg gtc gcc gcc atc aag gaa acc gag aag atg	963			
Gly Ser Arg Ala Leu Val Val Ala Ala Ile Lys Glu Thr Glu Lys Met				
225	230	235		
acc ttc tcc cag ttc ctg gag gcc tat gag gac gtt gtg gca cgc tcc	1011			
Thr Phe Ser Gln Phe Leu Glu Ala Tyr Glu Asp Val Val Ala Arg Ser				
240	245	250		
cgc gtc ggc aag ctc acc atg gat gac tac cag ggt gtc acc atc tcc	1059			
Arg Val Gly Lys Leu Thr Met Asp Asp Tyr Gln Gly Val Thr Ile Ser				
255	260	265	270	
ttg acc aac ccg ggt ggc atc ggt acc cgc cac tcc atc ccg cgt ctg	1107			
Leu Thr Asn Pro Gly Gly Ile Gly Thr Arg His Ser Ile Pro Arg Leu				
275	280	285		
acc aag ggc cag ggc acc atc atc ggt gtc ggt tcc atg gac tac ccg	1155			
Thr Lys Gly Gln Gly Thr Ile Ile Gly Val Gly Ser Met Asp Tyr Pro				
290	295	300		
gcc gag ttc cag ggt gcc tcc gag gac cgt ctc gcc gag ctc ggt gtg	1203			
Ala Glu Phe Gln Gly Ala Ser Glu Asp Arg Leu Ala Glu Leu Gly Val				
305	310	315		
ggc aag ctc gtc acc atc acc tcc acc tac gat cac cgc gtc atc cag	1251			
Gly Lys Leu Val Thr Ile Thr Ser Thr Tyr Asp His Arg Val Ile Gln				
320	325	330		
ggc gcg gaa tcc ggt gag ttc ctg cgc acc atg tcc cag ctg ctc gtg	1299			
Gly Ala Glu Ser Gly Glu Phe Leu Arg Thr Met Ser Gln Leu Leu Val				
335	340	345	350	
gac gat gcg ttc tgg gat cac atc ttc gag gag atg aac gtt ccc tac	1347			
Asp Asp Ala Phe Trp Asp His Ile Phe Glu Glu Met Asn Val Pro Tyr				
355	360	365		
acc ccg atg cgc tgg gca cag gac ctg ccc aac acc ggt gtc gac aag	1395			
Thr Pro Met Arg Trp Ala Gln Asp Leu Pro Asn Thr Gly Val Asp Lys				
370	375	380		
aac acc cgt atg cag ctc atc gag gcc tac cgc tcc cgc ggt cac	1443			
Asn Thr Arg Val Met Gln Leu Ile Glu Ala Tyr Arg Ser Arg Gly His				
385	390	395		
ctc atc gcc gac acc aac cca ctg ccc tgg gtc cag ccc ggc atg ccc	1491			
Leu Ile Ala Asp Thr Asn Pro Leu Pro Trp Val Gln Pro Gly Met Pro				
400	405	410		
gtc ccg gat cac cgt gac ctc gac atc gag acc cac ggc ctg acc ctg	1539			
Val Pro Asp His Arg Asp Leu Asp Ile Glu Thr His Gly Leu Thr Leu				
415	420	425	430	
tgg gat ctg gac cgt acc ttc cac gtc ggt ggt ttc ggt ggc aag gag	1587			
Trp Asp Leu Asp Arg Thr Phe His Val Gly Gly Phe Gly Gly Lys Glu				
435	440	445		

acc	atg	acc	ctg	cgc	gag	gtg	ctc	agc	cgc	ctc	cgc	gcc	gcc	tac	acc	1635
Thr	Met	Thr	Leu	Arg	Glu	Val	Leu	Ser	Arg	Leu	Arg	Ala	Ala	Tyr	Thr	
450								455						460		
ctc	aag	gtc	ggc	tcc	gag	tac	acc	cac	atc	ctc	gac	cgc	gat	gag	cgc	1683
Leu	Lys	Val	Gly	Ser	Glu	Tyr	Thr	His	Ile	Leu	Asp	Arg	Asp	Glu	Arg	
465							470					475				
acc	tgg	ctg	cag	gac	cgc	ctc	gag	gcc	ggt	atg	ccc	aag	ccc	acc	gcc	1731
Thr	Trp	Leu	Gln	Asp	Arg	Leu	Glu	Ala	Gly	Met	Pro	Lys	Pro	Thr	Ala	
480							485			490						
gcc	gag	cag	aag	tac	atc	ctg	cag	aag	ctc	aac	gcc	gcc	gag	gca	ttc	1779
Ala	Glu	Gln	Lys	Tyr	Ile	Leu	Gln	Lys	Leu	Asn	Ala	Ala	Glu	Ala	Phe	
495							500			505			510			
gag	aac	ttc	ctg	cag	acc	aag	tac	gtc	ggc	cag	aag	cgt	ttc	tcc	ctc	1827
Glu	Asn	Phe	Leu	Gln	Thr	Lys	Tyr	Val	Gly	Gln	Lys	Arg	Phe	Ser	Leu	
							515			520			525			
gag	ggt	gcc	gag	tca	ctg	atc	ccg	ctg	atg	gac	tcc	gcc	atc	gac	acc	1875
Glu	Gly	Ala	Glu	Ser	Leu	Ile	Pro	Leu	Met	Asp	Ser	Ala	Ile	Asp	Thr	
							530			535			540			
gcc	gca	ggc	cag	ggc	ctt	gac	gag	gtc	gtc	atc	ggc	atg	ccc	cac	cgt	1923
Ala	Ala	Gly	Gln	Gly	Leu	Asp	Glu	Val	Val	Ile	Gly	Met	Pro	His	Arg	
							545			550			555			
ggt	cgc	ctc	aac	gtg	ctg	ttc	aac	atc	gtc	ggc	aag	cca	ctg	gcc	tcg	1971
Gly	Arg	Leu	Asn	Val	Leu	Phe	Asn	Ile	Val	Gly	Lys	Pro	Leu	Ala	Ser	
							560			565			570			
atc	ttc	aac	gag	ttc	gag	ggc	cag	atg	gag	cag	ggc	cag	atc	ggt	ggc	2019
Ile	Phe	Asn	Glu	Phe	Glu	Gly	Gln	Met	Glu	Gln	Gly	Gln	Ile	Gly	Gly	
							575			580			585			590
tcc	ggt	gac	gtg	aag	tac	cac	ctc	ggt	tcc	gag	ggc	acc	cac	ctg	cag	2067
Ser	Gly	Asp	Val	Lys	Tyr	His	Leu	Gly	Ser	Glu	Gly	Thr	His	Leu	Gln	
							595			600			605			
atg	ttc	ggc	gac	ggc	gag	atc	aag	gtc	tcc	ctc	acc	gcc	aac	ccc	tcc	2115
Met	Phe	Gly	Asp	Gly	Glu	Ile	Lys	Val	Ser	Leu	Thr	Ala	Asn	Pro	Ser	
							610			615			620			
cac	ctc	gag	gcc	gtc	aac	ccg	gtc	gtg	gag	ggc	atc	gtc	cgc	gcc	aag	2163
His	Leu	Glu	Ala	Val	Asn	Pro	Val	Val	Glu	Gly	Ile	Val	Arg	Ala	Lys	
							625			630			635			
cag	gac	atc	ctg	gac	aag	ggc	ccg	gac	ggc	tac	acc	gtc	gtc	ccg	ctg	2211
Gln	Asp	Ile	Leu	Asp	Lys	Gly	Pro	Asp	Gly	Tyr	Thr	Val	Val	Pro	Leu	
							640			645			650			
ctg	ctc	cac	ggt	gac	gcc	gcc	ttc	gcc	ggc	ctg	ggc	atc	gtg	ccc	gag	2259
Leu	Leu	His	Gly	Asp	Ala	Ala	Phe	Ala	Gly	Leu	Gly	Ile	Val	Pro	Glu	
							655			660			665			670
acc	atc	aac	ctc	gca	gcc	ctg	cgt	ggt	tac	gat	gtc	ggt	ggc	acc	atc	2307
Thr	Ile	Asn	Leu	Ala	Ala	Leu	Arg	Gly	Tyr	Asp	Val	Gly	Gly	Thr	Ile	
							675			680			685			
cac	atc	gtg	gtc	aac	aac	cag	atc	ggc	ttc	acc	acc	acc	ccg	gac	tcc	2355
His	Ile	Val	Val	Asn	Asn	Gln	Ile	Gly	Phe	Thr	Thr	Thr	Pro	Asp	Ser	
							690			695			700			
agc	cgt	tcc	atg	cac	tac	gcc	acc	gac	tgc	gcc	aag	gcc	ttc	ggt	tgc	2403
Ser	Arg	Ser	Met	His	Tyr	Ala	Thr	Asp	Cys	Ala	Lys	Ala	Phe	Gly	Cys	
							705			710			715			

ccg	gtg	ttc	cac	gtc	aac	ggt	gac	gac	ccc	gag	gct	gtg	gtc	tgg	gtc	2451
Pro	Val	Phe	His	Val	Asn	Gly	Asp	Asp	Pro	Glu	Ala	Val	Val	Trp	Val	
720						725					730					
ggc	cag	ctg	gcc	acc	gag	tac	cgt	cgc	cgc	ttc	ggc	aag	gat	gtc	ttc	2499
Gly	Gln	Leu	Ala	Thr	Glu	Tyr	Arg	Arg	Arg	Phe	Gly	Lys	Asp	Val	Phe	
735						740					745				750	
atc	gac	ctc	atc	tgc	tac	cgc	ctg	cgc	ggc	cac	aac	gag	gct	gat	gac	2547
Ile	Asp	Leu	Ile	Cys	Tyr	Arg	Leu	Arg	Gly	His	Asn	Glu	Ala	Asp	Asp	
						755				760				765		
cca	tcc	atg	acc	cag	ccg	aag	atg	tac	gag	ctg	atc	acc	ggc	cgc	gac	2595
Pro	Ser	Met	Thr	Gln	Pro	Lys	Met	Tyr	Glu	Leu	Ile	Thr	Gly	Arg	Asp	
						770				775				780		
tcc	gtg	cgt	gcc	acc	tac	acc	gag	gac	ctc	ctc	ggc	cgt	ggt	gac	ctc	2643
Ser	Val	Arg	Ala	Thr	Tyr	Thr	Glu	Asp	Leu	Leu	Gly	Arg	Gly	Asp	Leu	
						785				790				795		
tcc	ccc	gag	gac	gcc	gag	gcc	gtt	gtc	cgc	gac	ttc	cac	gac	cag	atg	2691
Ser	Pro	Glu	Asp	Ala	Glu	Ala	Val	Val	Arg	Asp	Phe	His	Asp	Gln	Met	
						800				805				810		
gaa	tcc	gtg	ttc	aac	gag	gtc	aag	gaa	gcc	ggc	aag	aag	cag	cct	gat	2739
Glu	Ser	Val	Phe	Asn	Glu	Val	Lys	Glu	Ala	Gly	Lys	Lys	Gln	Pro	Asp	
						815				820				825		830
gag	cag	acc	ggc	atc	acc	ggt	tcc	cag	gaa	ctg	acc	cgt	ggc	ctg	gac	2787
Glu	Gln	Thr	Gly	Ile	Thr	Gly	Ser	Gln	Glu	Leu	Thr	Arg	Gly	Leu	Asp	
						835				840				845		
acc	aac	atc	acc	cgc	gag	gaa	ctg	gtc	gaa	ctc	ggc	cag	gcc	ttc	gtc	2835
Thr	Asn	Ile	Thr	Arg	Glu	Glu	Leu	Val	Glu	Leu	Gly	Gln	Ala	Phe	Val	
						850				855				860		
aac	acc	cca	gag	ggc	tcc	acc	tac	cac	cca	cgt	gtg	gca	ccg	gtg	gcc	2883
Asn	Thr	Pro	Glu	Gly	Phe	Thr	Tyr	His	Pro	Arg	Val	Ala	Pro	Val	Ala	
						865				870				875		
aag	aag	cgt	gcc	gag	tcc	gtc	acc	gag	ggt	ggc	atc	gac	tgg	gca	tgg	2931
Lys	Lys	Arg	Ala	Glu	Ser	Val	Thr	Glu	Gly	Gly	Ile	Asp	Trp	Ala	Trp	
						880				885				890		
ggc	gag	ctc	atc	gcc	tcc	ggc	tcc	ctg	gcc	acc	tcc	ggc	agg	ctg	gtc	2979
Gly	Glu	Leu	Ile	Ala	Phe	Gly	Ser	Leu	Ala	Thr	Ser	Gly	Arg	Leu	Val	
						895				900				905		910
cgc	ctc	gcc	ggt	gag	gat	tcc	cgc	cgt	ggt	acc	ttc	acc	cag	cgt	cac	3027
Arg	Leu	Ala	Gly	Glu	Asp	Ser	Arg	Arg	Gly	Thr	Phe	Thr	Gln	Arg	His	
						915				920				925		
gcc	gtg	gcc	atc	gac	ccg	aac	acc	gcc	gag	gag	tcc	aac	ccg	ctc	cac	3075
Ala	Val	Ala	Ile	Asp	Pro	Asn	Thr	Ala	Glu	Glu	Phe	Asn	Pro	Leu	His	
						930				935				940		
gag	ctg	gca	cag	gcc	aag	ggc	ggc	ggc	aag	tcc	ctc	gtc	tac	aac	tcc	3123
Glu	Leu	Ala	Gln	Ala	Lys	Gly	Gly	Gly	Lys	Phe	Leu	Val	Tyr	Asn	Ser	
						945				950				955		
gcg	ctg	acc	gag	tac	gcg	ggt	atg	ggc	tcc	gaa	tac	ggc	tac	tcc	gtg	3171
Ala	Leu	Thr	Glu	Tyr	Ala	Gly	Met	Gly	Phe	Glu	Tyr	Gly	Tyr	Ser	Val	
						960				965				970		
ggc	aac	ccg	gac	gcc	gtg	gtg	tcc	tgg	gag	gca	cag	ttc	ggt	gac	ttc	3219
Gly	Asn	Pro	Asp	Ala	Val	Val	Ser	Trp	Glu	Ala	Gln	Phe	Gly	Asp	Phe	
						975				980				985		990

gcc aac ggt gca cag acc atc atc gat gag tac atc tcc tcc ggt gag	3267
Ala Asn Gly Ala Gln Thr Ile Ile Asp Glu Tyr Ile Ser Ser Gly Glu	
995 1000 1005	
gcc aag tgg ggc cag acc tcc tcg gtc atc ctg ctg ctg ccc cac ggt	3315
Ala Lys Trp Gly Gln Thr Ser Ser Val Ile Leu Leu Leu Pro His Gly	
1010 1015 1020	
tac gag ggc cag ggt ccg gac cac tcc tcc gca cgc atc gag cgt ttc	3363
Tyr Glu Gly Gln Gly Pro Asp His Ser Ser Ala Arg Ile Glu Arg Phe	
1025 1030 1035	
ctg cag ctg tgc gcc gag ggt tcc atg acc atc gcc cag ccg acc acc	3411
Leu Gln Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln Pro Thr Thr	
1040 1045 1050	
ccg gcg aac tac ttc cac ctg ctg cgt cgt cac gca ctg ggc aag atg	3459
Pro Ala Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu Gly Lys Met	
1055 1060 1065 1070	
aag cgc ccg ctg gtc gtc ttc acc ccg aag tcc atg ctg cgc aac aag	3507
Lys Arg Pro Leu Val Val Phe Thr Pro Lys Ser Met Leu Arg Asn Lys	
1075 1080 1085	
gcc gcc acc tcc gct ccg gag gag ttc acc gag gtc acc cgc ttc aag	3555
Ala Ala Thr Ser Ala Pro Glu Glu Phe Thr Glu Val Thr Arg Phe Lys	
1090 1095 1100	
tcc gtg atc gac gat ccg aac gtg gcg gat gcc tcc aag gtg aag aag	3603
Ser Val Ile Asp Asp Pro Asn Val Ala Asp Ala Ser Lys Val Lys Lys	
1105 1110 1115	
atc atg ctg tgc tcc ggc aag atc tac tac gaa ctg gcc aag cgc aag	3651
Ile Met Leu Cys Ser Gly Lys Ile Tyr Tyr Glu Leu Ala Lys Arg Lys	
1120 1125 1130	
gag aag gac aac cgc gac gac atc gcg atc gtg cgc atc gag atg ctg	3699
Glu Lys Asp Asn Arg Asp Asp Ile Ala Ile Val Arg Ile Glu Met Leu	
1135 1140 1145 1150	
cac ccg atc ccg ttc aac cgt ctg cgc gac gcc ttc gac ggc tac ccc	3747
His Pro Ile Pro Phe Asn Arg Leu Arg Asp Ala Phe Asp Gly Tyr Pro	
1155 1160 1165	
aac gcc gag gag atc ctg ttc gtt cag gac gag ccg gca aac cag ggt	3795
Asn Ala Glu Glu Ile Leu Phe Val Gln Asp Glu Pro Ala Asn Gln Gly	
1170 1175 1180	
gcc tgg ccg ttc tac cag gag cac ctg ccc aac ctc atc gag ggc atg	3843
Ala Trp Pro Phe Tyr Gln Glu His Leu Pro Asn Leu Ile Glu Gly Met	
1185 1190 1195	
ctc ccg atg cgt cgc atc tcg cgc cgt tcc cag tcc tcg act gcg acc	3891
Leu Pro Met Arg Arg Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr	
1200 1205 1210	
ggt atc gcg aag gtg cac acc atc gag cag cag aag ctg ctg gat gat	3939
Gly Ile Ala Lys Val His Thr Ile Glu Gln Gln Lys Leu Leu Asp Asp	
1215 1220 1225 1230	
gcg ttc aac gca taaacgttaa tacagcggtt gataccttga accccgcccgc	3991
Ala Phe Asn Ala	
accctttaga tgcggcgccc gtttgcttt gcctgcatacg gcgataatat tcatacacac	4051
ccatcacgtt taagttctgc atttggatcg tgcgagcatc ccgggt	4096

<211> 1234

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 34

Val	Ser	Ser	Ala	Ser	Thr	Phe	Gly	Gln	Asn	Ala	Trp	Leu	Val	Asp	Glu
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Met	Phe	Gln	Gln	Phe	Lys	Lys	Asp	Pro	Gln	Ser	Val	Asp	Lys	Glu	Trp
				20				25					30		
Arg	Glu	Leu	Phe	Glu	Ser	Gln	Gly	Gly	Pro	Gln	Ala	Glu	Lys	Ala	Thr
				35			40					45			
Pro	Ala	Thr	Pro	Glu	Ala	Lys	Lys	Ala	Ala	Ser	Ser	Gln	Ser	Ser	Thr
				50		55				60					
Ser	Gly	Gln	Ser	Thr	Ala	Lys	Ala	Ala	Pro	Ala	Ala	Lys	Thr	Ala	Pro
				65		70			75				80		
Ala	Ser	Ala	Pro	Ala	Lys	Ala	Ala	Pro	Val	Lys	Gln	Asn	Gln	Ala	Ser
					85			90				95			
Lys	Pro	Ala	Lys	Lys	Ala	Lys	Glu	Ser	Pro	Leu	Ser	Lys	Pro	Ala	Ala
				100			105					110			
Met	Pro	Glu	Pro	Gly	Thr	Thr	Pro	Leu	Arg	Gly	Ile	Phe	Lys	Ser	Ile
				115			120				125				
Ala	Lys	Asn	Met	Asp	Leu	Ser	Leu	Glu	Val	Pro	Thr	Ala	Thr	Ser	Val
				130			135				140				
Arg	Asp	Met	Pro	Ala	Arg	Leu	Met	Phe	Glu	Asn	Arg	Ala	Met	Val	Asn
				145		150			155				160		
Asp	Gln	Leu	Lys	Arg	Thr	Arg	Gly	Gly	Lys	Ile	Ser	Phe	Thr	His	Ile
				165			170				175				
Ile	Gly	Tyr	Ala	Met	Val	Lys	Ala	Val	Met	Ala	His	Pro	Asp	Met	Asn
				180			185				190				
Asn	Ser	Tyr	Asp	Ile	Val	Asp	Gly	Lys	Pro	Ser	Leu	Val	Val	Pro	Glu
				195			200				205				
His	Ile	Asn	Leu	Gly	Leu	Ala	Ile	Asp	Leu	Pro	Gln	Lys	Asp	Gly	Ser
				210			215				220				
Arg	Ala	Leu	Val	Val	Ala	Ala	Ile	Lys	Glu	Thr	Glu	Lys	Met	Thr	Phe
				225		230			235				240		
Ser	Gln	Phe	Leu	Glu	Ala	Tyr	Glu	Asp	Val	Val	Ala	Arg	Ser	Arg	Val
				245			250				255				
Gly	Lys	Leu	Thr	Met	Asp	Asp	Tyr	Gln	Gly	Val	Thr	Ile	Ser	Leu	Thr
				260			265				270				
Asn	Pro	Gly	Gly	Ile	Gly	Thr	Arg	His	Ser	Ile	Pro	Arg	Leu	Thr	Lys
				275			280				285				
Gly	Gln	Gly	Thr	Ile	Ile	Gly	Val	Gly	Ser	Met	Asp	Tyr	Pro	Ala	Glu
				290		295				300					
Phe	Gln	Gly	Ala	Ser	Glu	Asp	Arg	Leu	Ala	Glu	Leu	Gly	Val	Gly	Lys
				305		310			315				320		
Leu	Val	Thr	Ile	Thr	Ser	Thr	Tyr	Asp	His	Arg	Val	Ile	Gln	Gly	Ala
					325			330				335			
Glu	Ser	Gly	Glu	Phe	Leu	Arg	Thr	Met	Ser	Gln	Leu	Leu	Val	Asp	Asp
				340			345				350				
Ala	Phe	Trp	Asp	His	Ile	Phe	Glu	Glu	Met	Asn	Val	Pro	Tyr	Thr	Pro
				355			360				365				

Met Arg Trp Ala Gln Asp Leu Pro Asn Thr Gly Val Asp Lys Asn Thr  
 370 375 380  
 Arg Val Met Gln Leu Ile Glu Ala Tyr Arg Ser Arg Gly His Leu Ile  
 385 390 395 400  
 Ala Asp Thr Asn Pro Leu Pro Trp Val Gln Pro Gly Met Pro Val Pro  
 405 410 415  
 Asp His Arg Asp Leu Asp Ile Glu Thr His Gly Leu Thr Leu Trp Asp  
 420 425 430  
 Leu Asp Arg Thr Phe His Val Gly Gly Phe Gly Gly Lys Glu Thr Met  
 435 440 445  
 Thr Leu Arg Glu Val Leu Ser Arg Leu Arg Ala Ala Tyr Thr Leu Lys  
 450 455 460  
 Val Gly Ser Glu Tyr Thr His Ile Leu Asp Arg Asp Glu Arg Thr Trp  
 465 470 475 480  
 Leu Gln Asp Arg Leu Glu Ala Gly Met Pro Lys Pro Thr Ala Ala Glu  
 485 490 495  
 Gln Lys Tyr Ile Leu Gln Lys Leu Asn Ala Ala Glu Ala Phe Glu Asn  
 500 505 510  
 Phe Leu Gln Thr Lys Tyr Val Gly Gln Lys Arg Phe Ser Leu Glu Gly  
 515 520 525  
 Ala Glu Ser Leu Ile Pro Leu Met Asp Ser Ala Ile Asp Thr Ala Ala  
 530 535 540  
 Gly Gln Gly Leu Asp Glu Val Val Ile Gly Met Pro His Arg Gly Arg  
 545 550 555 560  
 Leu Asn Val Leu Phe Asn Ile Val Gly Lys Pro Leu Ala Ser Ile Phe  
 565 570 575  
 Asn Glu Phe Glu Gly Gln Met Glu Gln Gly Gln Ile Gly Gly Ser Gly  
 580 585 590  
 Asp Val Lys Tyr His Leu Gly Ser Glu Gly Thr His Leu Gln Met Phe  
 595 600 605  
 Gly Asp Gly Glu Ile Lys Val Ser Leu Thr Ala Asn Pro Ser His Leu  
 610 615 620  
 Glu Ala Val Asn Pro Val Val Glu Gly Ile Val Arg Ala Lys Gln Asp  
 625 630 635 640  
 Ile Leu Asp Lys Gly Pro Asp Gly Tyr Thr Val Val Pro Leu Leu Leu  
 645 650 655  
 His Gly Asp Ala Ala Phe Ala Gly Leu Gly Ile Val Pro Glu Thr Ile  
 660 665 670  
 Asn Leu Ala Ala Leu Arg Gly Tyr Asp Val Gly Gly Thr Ile His Ile  
 675 680 685  
 Val Val Asn Asn Gln Ile Gly Phe Thr Thr Pro Asp Ser Ser Arg  
 690 695 700  
 Ser Met His Tyr Ala Thr Asp Cys Ala Lys Ala Phe Gly Cys Pro Val  
 705 710 715 720  
 Phe His Val Asn Gly Asp Asp Pro Glu Ala Val Val Trp Val Gly Gln  
 725 730 735  
 Leu Ala Thr Glu Tyr Arg Arg Arg Phe Gly Lys Asp Val Phe Ile Asp  
 740 745 750  
 Leu Ile Cys Tyr Arg Leu Arg Gly His Asn Glu Ala Asp Asp Pro Ser  
 755 760 765  
 Met Thr Gln Pro Lys Met Tyr Glu Leu Ile Thr Gly Arg Asp Ser Val

770	775	780
Arg Ala Thr Tyr Thr Glu Asp Leu Leu Gly Arg	Gly Asp Leu Ser Pro	
785 790	795	800
Glu Asp Ala Glu Ala Val Val Arg Asp Phe His	Asp Gln Met Glu Ser	
805	810	815
Val Phe Asn Glu Val Lys Glu Ala Gly Lys Lys	Gln Pro Asp Glu Gln	
820	825	830
Thr Gly Ile Thr Gly Ser Gln Glu Leu Thr Arg	Gly Leu Asp Thr Asn	
835	840	845
Ile Thr Arg Glu Glu Leu Val Glu Leu Gly Gln	Ala Phe Val Asn Thr	
850	855	860
Pro Glu Gly Phe Thr Tyr His Pro Arg Val Ala	Pro Val Ala Lys Lys	
865 870	875	880
Arg Ala Glu Ser Val Thr Glu Gly Gly Ile Asp	Trp Ala Trp Gly Glu	
885	890	895
Leu Ile Ala Phe Gly Ser Leu Ala Thr Ser Gly	Arg Leu Val Arg Leu	
900	905	910
Ala Gly Glu Asp Ser Arg Arg Gly Thr Phe Thr	Gln Arg His Ala Val	
915	920	925
Ala Ile Asp Pro Asn Thr Ala Glu Glu Phe Asn	Pro Leu His Glu Leu	
930	935	940
Ala Gln Ala Lys Gly Gly Lys Phe Leu Val Tyr	Asn Ser Ala Leu	
945 950	955	960
Thr Glu Tyr Ala Gly Met Gly Phe Glu Tyr Gly	Tyr Ser Val Gly Asn	
965	970	975
Pro Asp Ala Val Val Ser Trp Glu Ala Gln Phe	Gly Asp Phe Ala Asn	
980	985	990
Gly Ala Gln Thr Ile Ile Asp Glu Tyr Ile Ser	Ser Gly Glu Ala Lys	
995	1000	1005
Trp Gly Gln Thr Ser Ser Val Ile Leu Leu Leu	Pro His Gly Tyr Glu	
1010 1015	1020	
Gly Gln Gly Pro Asp His Ser Ser Ala Arg Ile	Glu Arg Phe Leu Gln	
1025 1030	1035	1040
Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln	Pro Thr Thr Pro Ala	
1045	1050	1055
Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu	Gly Lys Met Lys Arg	
1060	1065	1070
Pro Leu Val Val Phe Thr Pro Lys Ser Met Leu	Arg Asn Lys Ala Ala	
1075	1080	1085
Thr Ser Ala Pro Glu Glu Phe Thr Glu Val Thr	Arg Phe Lys Ser Val	
1090 1095	1100	
Ile Asp Asp Pro Asn Val Ala Asp Ala Ser Lys	Val Lys Lys Ile Met	
1105 1110	1115	1120
Leu Cys Ser Gly Lys Ile Tyr Tyr Glu Leu Ala	Lys Arg Lys Glu Lys	
1125	1130	1135
Asp Asn Arg Asp Asp Ile Ala Ile Val Arg Ile	Glu Met Leu His Pro	
1140	1145	1150
Ile Pro Phe Asn Arg Leu Arg Asp Ala Phe Asp	Gly Tyr Pro Asn Ala	
1155	1160	1165
Glu Glu Ile Leu Phe Val Gln Asp Glu Pro Ala	Asn Gln Gly Ala Trp	
1170	1175	1180

Pro Phe Tyr Gln Glu His Leu Pro Asn Leu Ile Glu Gly Met Leu Pro  
1185 1190 1195 1200  
Met Arg Arg Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr Gly Ile  
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Ala Lys Val His Thr Ile Glu Gln Gln Lys Leu Leu Asp Asp Ala Phe  
1220 1225 1230  
Asn Ala

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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer for aceA

<400> 35  
cctctaccca gcgaactccg 20

<210> 36  
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<220>  
<223> Description of Artificial Sequence: primer for aceA

<400> 36  
ctgccttgaa ctcacggttc 20

<210> 37  
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<220>  
<223> Description of Artificial Sequence: primer for accBC

<400> 37  
catccacccccc ggctacggct 20

<210> 38  
<211> 20  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer for accBC

<400> 38  
cggtgactgg gtgttccacc 20

<210> 39  
<211> 20  
<212> DNA  
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<220>  
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acggcccagc cctgaccgac 20

<210> 40  
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<220>  
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<400> 40  
agcagcgccc atgacggcga 20

<210> 41  
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<220>  
<223> Description of Artificial Sequence: primer for dtsR2

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acggcccagc cctgaccgac 20

<210> 42  
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<223> Description of Artificial Sequence: primer for dtsR2

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agcagcgccc atgacggcga 20

<210> 43  
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<223> Description of Artificial Sequence: primer for pfk

<400> 43  
cgtcatccga ggaatcggtcc 20

<210> 44  
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<220>

<223> Description of Artificial Sequence: primer for pfk

<400> 44  
cgtggcggcc catgacacctcc 20

<210> 45  
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<212> DNA  
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<223> Description of Artificial Sequence: primer for scrB

<220>

<221> misc\_feature  
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<400> 45  
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<210> 46  
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<223> Description of Artificial Sequence: primer for scrB

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<400> 46  
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<210> 47  
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for gluABCD

<400> 47  
ccatccggat ccggcaagtc 20

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for gluABCD

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<210> 49

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pdhA

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<210> 50

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pdhA

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<210> 51

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pc

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<210> 52  
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<400> 52  
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<210> 53  
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<223> Description of Artificial Sequence: primer for ppc

<400> 53  
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<210> 54  
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<220>  
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<400> 54  
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<210> 55  
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<212> DNA  
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<223> Description of Artificial Sequence: primer for acn

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<222> (3)..(3)  
<223> n = inosine

<220>  
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<400> 55  
gtnggnacng aytcscatac 20

<210> 56  
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<220>  
<223> Description of Artificial Sequence: primer for acn

<220>  
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<223> n = inosine

<220>  
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<222> (9)..(9)  
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<220>  
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<400> 56  
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<210> 57  
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<223> Description of Artificial Sequence: primer for icd

<400> 57  
gacatttcac tcgctggacg 20

<210> 58  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer for icd  
  
<400> 58  
ccgtactttt cagccttctg 20  
  
<210> 59  
<211> 17  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer for lpd  
  
<400> 59  
atcatcgcaa ccggttc 17  
  
<210> 60  
<211> 19  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer for lpd  
  
<400> 60  
cgtcaccgat ggcgtaaat 19  
  
<210> 61  
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<223> Description of Artificial Sequence: primer for odhA  
  
<400> 61  
acaccgtggt cgcctcaacg 20  
  
<210> 62  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
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<400> 62  
tgctaaccgg tcccacctgg 20  
  
<210> 63

<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer for screening PCR of lpd

<400> 63  
tacgaggagc agatcctcaa 20

<210> 64  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer for screening PCR of lpd

<400> 64  
ttgacgcccgg tggttctccag 20

<210> 65  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer for LA cloning of acn

<400> 65  
ggtaaagcta agtagtttagc 20

<210> 66  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer for LA cloning of acn

<400> 66  
agctactaaa cctgcacc 18

<210> 67  
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<220>  
<223> Description of Artificial Sequence: primer for  
LA cloning of icd

<400> 67  
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<210> 68  
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<212> DNA  
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<223> Description of Artificial Sequence: primer for  
LA cloning of icd

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<210> 69  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer for  
LA cloning of lpd

<400> 69  
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<210> 70  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer for  
LA cloning of lpd

<400> 70  
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<210> 71  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer for

LA cloning of acn

<400> 71  
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<210> 72  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer for  
LA cloning of acn

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<210> 73  
<211> 18  
<212> DNA  
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<223> Description of Artificial Sequence: primer for  
LA cloning of icd

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<210> 74  
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<223> Description of Artificial Sequence: primer for  
LA cloning of icd

<400> 74  
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<210> 75  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer for  
LA cloning of odhA

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<212> DNA  
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<223> Description of Artificial Sequence: primer for  
LA cloning of odhA  
  
<400> 76  
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<210> 77  
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<212> DNA  
  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer for  
amplifying gdh gene  
  
<400> 77  
gcgcctgcag gtccgagggt gtgcgttcgg ca 32  
  
<210> 78  
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<212> DNA  
  
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amplifying gdh gene  
  
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gcgcctgcag ccaccagga tgccctcaacc ag 32  
  
<210> 79  
<211> 1344  
<212> DNA  
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<222> (1)..(1341)  
  
<400> 79

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Met	Thr	Val	Asp	Glu	Gln	Val	Ser	Asn	Tyr	Tyr	Asp	Met	Leu	Leu	Lys	
1				5					10					15		
cgc	aac	gcc	ggg	gaa	cct	gag	ttc	cac	cag	gct	gtc	gcg	gag	gtt	ctc	96
Arg	Asn	Ala	Gly	Glu	Pro	Glu	Phe	His	Gln	Ala	Val	Ala	Glu	Val	Leu	
				20					25				30			
gaa	tct	ctg	aag	atc	gtc	ctg	gag	aag	gac	ccg	cac	tac	gcc	gac	tac	144
Glu	Ser	Leu	Lys	Ile	Val	Leu	Glu	Lys	Asp	Pro	His	Tyr	Ala	Asp	Tyr	
				35				40				45				
ggt	ctg	atc	cag	cgt	ctc	tgc	gaa	ccg	gaa	cgc	cag	ctg	atc	ttc	cgt	192
Gly	Leu	Ile	Gln	Arg	Ile	Cys	Glu	Pro	Glu	Arg	Gln	Leu	Ile	Phe	Arg	
				50				55			60					
gtg	ccc	tgg	gtg	gat	gac	aac	ggt	cag	gtg	cac	gtc	aac	cgt	ggt	ttc	240
Val	Pro	Trp	Val	Asp	Asp	Asn	Gly	Gln	Val	His	Val	Asn	Arg	Gly	Phe	
				65				70			75			80		
cgt	gtc	cag	ttc	aac	tcc	gca	ctc	ggc	ccg	tac	aag	ggt	ggt	ctg	cgt	288
Arg	Val	Gln	Phe	Asn	Ser	Ala	Leu	Gly	Pro	Tyr	Lys	Gly	Gly	Leu	Arg	
				85				90				95				
ttc	cac	ccc	tcc	gtc	aac	ctc	ggc	atc	gtc	aag	ttc	ctc	ggc	ttc	gag	336
Phe	His	Pro	Ser	Val	Asn	Leu	Gly	Ile	Val	Lys	Phe	Leu	Gly	Phe	Glu	
				100				105				110				
cag	atc	ttc	aag	aac	tcc	ctc	acc	ggt	ctg	ccg	atc	ggt	ggc	ggc	aag	384
Gln	Ile	Phe	Lys	Asn	Ser	Leu	Thr	Gly	Leu	Pro	Ile	Gly	Gly	Gly	Lys	
				115				120			125					
ggt	ggt	tcc	gac	ttc	gac	ccg	aag	ggc	aag	tcc	gag	ctg	gag	atc	atg	432
Gly	Gly	Ser	Asp	Phe	Asp	Pro	Lys	Gly	Lys	Ser	Glu	Leu	Glu	Ile	Met	
				130				135			140					
cgc	ttc	tgc	cag	tcc	ttc	atg	acc	gag	ctg	cac	cgc	cac	atc	ggc	gag	480
Arg	Phe	Cys	Gln	Ser	Phe	Met	Thr	Glu	Leu	His	Arg	His	Ile	Gly	Glu	
				145				150			155			160		
tac	cg	gat	gtc	ccg	gcc	ggt	gac	atc	gga	gtc	ggt	ggc	cgc	gag	atc	528
Tyr	Arg	Asp	Val	Pro	Ala	Gly	Asp	Ile	Gly	Val	Gly	Gly	Arg	Glu	Ile	
				165				170			175					
ggt	tac	ctc	ttc	ggc	cac	tac	cgc	cgt	ctg	gcc	aac	cag	cac	gag	tcc	576
Gly	Tyr	Leu	Phe	Gly	His	Tyr	Arg	Arg	Leu	Ala	Asn	Gln	His	Glu	Ser	
				180				185			190					
ggt	gt	ctc	acc	ggc	aag	ggc	ctg	acc	tgg	ggt	ggt	tcc	ctg	gtc	cgc	624
Gly	Val	Leu	Thr	Gly	Lys	Gly	Leu	Thr	Trp	Gly	Gly	Ser	Leu	Val	Arg	
				195				200			205					
acc	gag	gcc	acc	ggc	tcc	ggc	acc	gtc	tac	tcc	gtc	cag	gag	atg	atc	672
Thr	Glu	Ala	Thr	Gly	Phe	Gly	Thr	Val	Tyr	Phe	Val	Gln	Glu	Met	Ile	
				210				215			220					
aag	gcg	gaa	ggg	gag	acc	ctc	gag	ggc	aag	aag	gtc	atc	gtc	tcc	ggt	720
Lys	Ala	Glu	Gly	Glu	Thr	Leu	Glu	Gly	Lys	Lys	Val	Ile	Val	Ser	Gly	
				225				230			235			240		
tcc	ggc	aac	gt	gcc	acc	tac	gcc	atc	cag	aag	gt	cag	gaa	ctg	ggt	768
Ser	Gly	Asn	Val	Ala	Thr	Tyr	Ala	Ile	Gln	Lys	Val	Gln	Glu	Leu	Gly	
				245				250			255					
gcg	gtt	gt	gtc	ggc	tcc	tcc	gac	tcc	agc	ggc	tgg	gtc	tcc	acc	ccg	816
Ala	Val	Val	Val	Gly	Phe	Ser	Asp	Ser	Ser	Gly	Trp	Val	Ser	Thr	Pro	
				260				265			270					

aac	ggt	gtt	gac	gtg	gcc	aag	ctg	cgt	gag	atc	aag	gag	gtc	cgt	cgt	864
Asn	Gly	Val	Asp	Val	Ala	Lys	Leu	Arg	Glu	Ile	Lys	Glu	Val	Arg	Arg	
							275			280			285			
gca	cgc	gtg	tcc	tcc	tac	gcc	gac	gag	gtg	gag	ggt	gcg	gag	tac	cac	912
Ala	Arg	Val	Ser	Ser	Tyr	Ala	Asp	Glu	Val	Glu	Gly	Ala	Glu	Tyr	His	
							290			295			300			
acc	gac	ggc	tcc	atc	tgg	gat	ctg	acc	gcc	gac	atc	gcg	ctg	ccc	tgc	960
Thr	Asp	Gly	Ser	Ile	Trp	Asp	Leu	Thr	Ala	Asp	Ile	Ala	Leu	Pro	Cys	
							305			310			315			320
gcc	acc	cag	aac	gaa	ctg	gac	ggc	gac	aac	gcc	cgc	acc	ctc	gcg	gac	1008
Ala	Thr	Gln	Asn	Glu	Leu	Asp	Gly	Asp	Asn	Ala	Arg	Thr	Leu	Ala	Asp	
							325			330			335			
aac	ggc	tgc	cgc	tcc	gtg	gcg	gag	ggc	gcc	aac	atg	ccc	tcc	acc	ccc	1056
Asn	Gly	Cys	Arg	Phe	Val	Ala	Glu	Gly	Ala	Asn	Met	Pro	Ser	Thr	Pro	
							340			345			350			
gag	gcc	atc	gac	gtc	tcc	cgt	gag	cgt	ggt	gtt	ctc	tcc	ggg	ccg	ggc	1104
Glu	Ala	Ile	Asp	Val	Phe	Arg	Glu	Arg	Gly	Val	Leu	Phe	Gly	Pro	Gly	
							355			360			365			
aag	gct	gcc	aac	gcc	ggt	ggc	gtg	gcc	acc	tcc	gcc	ctg	gag	atg	cag	1152
Lys	Ala	Ala	Asn	Ala	Gly	Gly	Val	Ala	Thr	Ser	Ala	Leu	Glu	Met	Gln	
							370			375			380			
cag	aac	gcc	tcc	cgt	gat	tcc	tgg	agc	tcc	gag	tac	acc	gat	gag	cgt	1200
Gln	Asn	Ala	Ser	Arg	Asp	Ser	Trp	Ser	Phe	Glu	Tyr	Thr	Asp	Glu	Arg	
							385			390			395			400
ctc	cac	cgc	atc	atg	aag	aac	atc	tcc	aag	tcc	tgc	gcc	gat	acc	gcc	1248
Leu	His	Arg	Ile	Met	Lys	Asn	Ile	Phe	Lys	Ser	Cys	Ala	Asp	Thr	Ala	
							405			410			415			
aag	gag	tac	ggc	cac	gag	aag	aac	tac	gtg	gtc	ggt	gcg	aac	atc	gcc	1296
Lys	Glu	Tyr	Gly	His	Glu	Lys	Asn	Tyr	Val	Val	Gly	Ala	Asn	Ile	Ala	
							420			425			430			
gga	tcc	aag	aag	gtc	gct	gac	gcc	atg	ctc	gcc	cag	ggt	gtc	atc	taa	1344
Gly	Phe	Lys	Lys	Val	Ala	Asp	Ala	Met	Leu	Ala	Gln	Gly	Val	Ile		
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<211> 447

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 80

Met	Thr	Val	Asp	Glu	Gln	Val	Ser	Asn	Tyr	Tyr	Asp	Met	Leu	Leu	Lys	
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Arg	Asn	Ala	Gly	Glu	Pro	Glu	Phe	His	Gln	Ala	Val	Ala	Glu	Val	Leu	
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Glu	Ser	Leu	Lys	Ile	Val	Leu	Glu	Lys	Asp	Pro	His	Tyr	Ala	Asp	Tyr	
								35			40			45		

Gly	Leu	Ile	Gln	Arg	Leu	Cys	Glu	Pro	Glu	Arg	Gln	Leu	Ile	Phe	Arg	
								50			55			60		

Val	Pro	Trp	Val	Asp	Asp	Asn	Gly	Gln	Val	His	Val	Asn	Arg	Gly	Phe	
								65			70			75		80

Arg	Val	Gln	Phe	Asn	Ser	Ala	Leu	Gly	Pro	Tyr	Lys	Gly	Gly	Leu	Arg	
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	85		90		95										
Phe	His	Pro	Ser	Val	Asn	Leu	Gly	Ile	Val	Lys	Phe	Leu	Gly	Phe	Glu
				100				105						110	
Gln	Ile	Phe	Lys	Asn	Ser	Leu	Thr	Gly	Leu	Pro	Ile	Gly	Gly	Gly	Lys
				115				120					125		
Gly	Gly	Ser	Asp	Phe	Asp	Pro	Lys	Gly	Lys	Ser	Glu	Leu	Glu	Ile	Met
				130				135				140			
Arg	Phe	Cys	Gln	Ser	Phe	Met	Thr	Glu	Leu	His	Arg	His	Ile	Gly	Glu
				145				150			155			160	
Tyr	Arg	Asp	Val	Pro	Ala	Gly	Asp	Ile	Gly	Val	Gly	Gly	Arg	Glu	Ile
								165			170			175	
Gly	Tyr	Leu	Phe	Gly	His	Tyr	Arg	Arg	Leu	Ala	Asn	Gln	His	Glu	Ser
				180				185					190		
Gly	Val	Leu	Thr	Gly	Lys	Gly	Leu	Thr	Trp	Gly	Gly	Ser	Leu	Val	Arg
				195				200					205		
Thr	Glu	Ala	Thr	Gly	Phe	Gly	Thr	Val	Tyr	Phe	Val	Gln	Glu	Met	Ile
				210				215				220			
Lys	Ala	Glu	Gly	Glu	Thr	Leu	Glu	Gly	Lys	Lys	Val	Ile	Val	Ser	Gly
				225				230			235			240	
Ser	Gly	Asn	Val	Ala	Thr	Tyr	Ala	Ile	Gln	Lys	Val	Gln	Glu	Leu	Gly
								245			250			255	
Ala	Val	Val	Val	Gly	Phe	Ser	Asp	Ser	Ser	Gly	Trp	Val	Ser	Thr	Pro
				260				265					270		
Asn	Gly	Val	Asp	Val	Ala	Lys	Leu	Arg	Glu	Ile	Lys	Glu	Val	Arg	Arg
				275				280				285			
Ala	Arg	Val	Ser	Ser	Tyr	Ala	Asp	Glu	Val	Glu	Gly	Ala	Glu	Tyr	His
				290				295			300				
Thr	Asp	Gly	Ser	Ile	Trp	Asp	Leu	Thr	Ala	Asp	Ile	Ala	Leu	Pro	Cys
				305				310			315			320	
Ala	Thr	Gln	Asn	Glu	Leu	Asp	Gly	Asp	Asn	Ala	Arg	Thr	Leu	Ala	Asp
								325			330			335	
Asn	Gly	Cys	Arg	Phe	Val	Ala	Glu	Gly	Ala	Asn	Met	Pro	Ser	Thr	Pro
				340				345					350		
Glu	Ala	Ile	Asp	Val	Phe	Arg	Glu	Arg	Gly	Val	Leu	Phe	Gly	Pro	Gly
				355				360				365			
Lys	Ala	Ala	Asn	Ala	Gly	Gly	Val	Ala	Thr	Ser	Ala	Leu	Glu	Met	Gln
				370				375				380			
Gln	Asn	Ala	Ser	Arg	Asp	Ser	Trp	Ser	Phe	Glu	Tyr	Thr	Asp	Glu	Arg
				385				390			395			400	
Leu	His	Arg	Ile	Met	Lys	Asn	Ile	Phe	Lys	Ser	Cys	Ala	Asp	Thr	Ala
								405			410			415	
Lys	Glu	Tyr	Gly	His	Glu	Lys	Asn	Tyr	Val	Val	Gly	Ala	Asn	Ile	Ala
				420				425				430			
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<210> 81  
 <211> 1344  
 <212> DNA  
 <213> Brevibacterium lactofermentum

<220>  
<221> CDS  
<222> (1)..(1341)

<400> 81

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cgc aat gct ggc gag cct gaa ttt cac cag gca gtg gca gag gtt ttg	96
Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu	
20 25 30	
gaa tct ttg aag atc gtc ctg gaa aag gac cct cat tac gct gat tac	144
Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr	
35 40 45	
ggt ctc atc cag cgc ctg tgc gag cct gag cgt cag ctc atc ttc cgt	192
Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg	
50 55 60	
gtg cct tgg gtt gat gac cag ggc cag gtc cac gtc aac cgt ggt ttc	240
Val Pro Trp Val Asp Asp Gln Gly Gln Val His Val Asn Arg Gly Phe	
65 70 75 80	
cgc gtg cag ttc aac tct gca ctt gga cca tac aag ggc ggc ctg cgc	288
Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg	
85 90 95	
ttc cac cca tct gta aac ctg ggc att gtg aag ttc ctg ggc ttt gag	336
Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu	
100 105 110	
cag atc ttt aaa aac tcc cta acc ggc ctg cca atc ggt ggt ggc aag	384
Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Lys	
115 120 125	
ggt gga tcc gac ttc gac cct aag ggc aag tcc gat ctg gaa atc atg	432
Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Asp Leu Glu Ile Met	
130 135 140	
cgt ttc tgc cag tcc ttc atg acc gag ctg cac cgc cac atc ggt gag	480
Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu	
145 150 155 160	
tac cgc gac gtt cct gca ggt gac atc gga gtt ggt ggc cgc gag atc	528
Tyr Arg Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile	
165 170 175	
ggt tac ctg ttt ggc cac tac cgt cgc atg gct aac cag cac gag tcc	576
Gly Tyr Leu Phe Gly His Tyr Arg Arg Met Ala Asn Gln His Glu Ser	
180 185 190	
ggc gtt ttg acc ggt aag ggc ctg acc tgg ggt gga tcc ctg gtc cgc	624
Gly Val Leu Thr Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg	
195 200 205	
acc gag gca act ggc tac ggc tgc gtt tac ttc gtg agt gaa atg atc	672
Thr Glu Ala Thr Gly Tyr Gly Cys Val Tyr Phe Val Ser Glu Met Ile	
210 215 220	
aag gct aag ggc gag agc atc agc ggc cag aag atc atc gtt tcc ggt	720
Lys Ala Lys Gly Glu Ser Ile Ser Gly Gln Lys Ile Ile Val Ser Gly	
225 230 235 240	
tcc ggc aac gta gca acc tac gcg att gaa aag gct cag gaa ctc ggc	768

Ser	Gly	Asn	Val	Ala	Thr	Tyr	Ala	Ile	Glu	Lys	Ala	Gln	Glu	Leu	Gly	
					245				250					255		
gca	acc	gtt	att	gtt	ttc	tcc	gat	tcc	agc	ggt	tgg	gtt	cat	acc	cct	816
Ala	Thr	Val	Ile	Gly	Phe	Ser	Asp	Ser	Ser	Gly	Trp	Val	His	Thr	Pro	
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aac	ggc	gtt	gac	gtg	gct	aag	ctc	cgc	gaa	atc	aag	gaa	gtt	cgc	cgc	864
Asn	Gly	Val	Asp	Val	Ala	Lys	Leu	Arg	Glu	Ile	Lys	Glu	Val	Arg	Arg	
					275				280				285			
gca	cgc	gta	tcc	gtg	tac	gcc	gac	gaa	att	gaa	ggc	gca	acc	tac	cac	912
Ala	Arg	Val	Ser	Val	Tyr	Ala	Asp	Glu	Ile	Glu	Gly	Ala	Thr	Tyr	His	
					290				295				300			
acc	gac	ggt	tcc	atc	tgg	gat	ctc	aag	tgc	gat	atc	gct	ctt	cct	tgt	960
Thr	Asp	Gly	Ser	Ile	Trp	Asp	Leu	Lys	Cys	Asp	Ile	Ala	Leu	Pro	Cys	
					305				310				315			320
gca	act	cag	aac	gag	ctc	aac	ggc	gag	aac	gct	aag	act	ctt	gca	gac	1008
Ala	Thr	Gln	Asn	Glu	Leu	Asn	Gly	Glu	Asn	Ala	Lys	Thr	Leu	Ala	Asp	
					325				330				335			
aac	ggc	tgc	cgt	ttc	gtt	gct	gaa	ggc	gcg	aac	atg	cct	tcc	acc	cct	1056
Asn	Gly	Cys	Arg	Phe	Val	Ala	Glu	Gly	Ala	Asn	Met	Pro	Ser	Thr	Pro	
					340				345				350			
gag	gct	gtt	gag	gtc	ttc	cgt	gag	cgc	gac	atc	cgc	ttc	gga	cca	ggc	1104
Glu	Ala	Val	Glu	Val	Phe	Arg	Glu	Arg	Asp	Ile	Arg	Phe	Gly	Pro	Gly	
					355				360				365			
aag	gca	gct	aac	gct	ggt	ggc	gtt	gca	acc	tcc	gct	ctg	gag	atg	cag	1152
Lys	Ala	Ala	Asn	Ala	Gly	Gly	Val	Ala	Thr	Ser	Ala	Leu	Glu	Met	Gln	
					370				375				380			
cag	aac	gct	tcg	cgc	gat	tcc	tgg	agc	ttc	gag	tac	acc	gac	gag	cgc	1200
Gln	Asn	Ala	Ser	Arg	Asp	Ser	Trp	Ser	Phe	Glu	Tyr	Thr	Asp	Glu	Arg	
					385				390				395			400
ctc	cag	gtg	atc	atg	aag	aac	atc	ttc	aag	acc	tgt	gca	gag	acc	gca	1248
Leu	Gln	Val	Ile	Met	Lys	Asn	Ile	Phe	Lys	Thr	Cys	Ala	Glu	Thr	Ala	
					405				410				415			
gca	gag	tat	gga	cac	gag	aac	gat	tac	gtt	gtc	ggc	gct	aac	att	gct	1296
Ala	Glu	Tyr	Gly	His	Glu	Asn	Asp	Tyr	Val	Val	Gly	Ala	Asn	Ile	Ala	
					420				425				430			
ggc	ttt	aag	aag	gta	gct	gac	gcg	atg	ctg	gca	cag	ggc	gtc	atc	taa	1344
Gly	Phe	Lys	Lys	Val	Ala	Asp	Ala	Met	Leu	Ala	Gln	Gly	Val	Ile		
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 <212> PRT  
 <213> Brevibacterium lactofermentum

<400> 82  
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 20 25 30  
 Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr  
 35 40 45

Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg  
 50 55 60  
 Val Pro Trp Val Asp Asp Gln Gly Gln Val His Val Asn Arg Gly Phe  
 65 70 75 80  
 Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg  
 85 90 95  
 Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu  
 100 105 110  
 Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys  
 115 120 125  
 Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Asp Leu Glu Ile Met  
 130 135 140  
 Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu  
 145 150 155 160  
 Tyr Arg Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile  
 165 170 175  
 Gly Tyr Leu Phe Gly His Tyr Arg Arg Met Ala Asn Gln His Glu Ser  
 180 185 190  
 Gly Val Leu Thr Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg  
 195 200 205  
 Thr Glu Ala Thr Gly Tyr Gly Cys Val Tyr Phe Val Ser Glu Met Ile  
 210 215 220  
 Lys Ala Lys Gly Glu Ser Ile Ser Gly Gln Lys Ile Ile Val Ser Gly  
 225 230 235 240  
 Ser Gly Asn Val Ala Thr Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly  
 245 250 255  
 Ala Thr Val Ile Gly Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro  
 260 265 270  
 Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg  
 275 280 285  
 Ala Arg Val Ser Val Tyr Ala Asp Glu Ile Glu Gly Ala Thr Tyr His  
 290 295 300  
 Thr Asp Gly Ser Ile Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys  
 305 310 315 320  
 Ala Thr Gln Asn Glu Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp  
 325 330 335  
 Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro  
 340 345 350  
 Glu Ala Val Glu Val Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly  
 355 360 365  
 Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln  
 370 375 380  
 Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg  
 385 390 395 400  
 Leu Gln Val Ile Met Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala  
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 Ala Glu Tyr Gly His Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala  
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aagatcacnt acatcgaygg 20  
  
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<210> 87  
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<210> 88  
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 <212> DNA

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<210> 89  
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 <213> Corynebacterium thermoaminogenes

<220>  
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 Val Ala Ser Asp Asn Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu  
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ttc gag atg ggc atc aag cag gcc acc gag ggt aac tcc ggt gtc atc 96  
 Phe Glu Met Gly Ile Lys Gln Ala Thr Glu Gly Asn Ser Gly Val Ile  
 20 25 30

ctg ggt aag atg ctg tcg gaa acc ggt ctg gtc acc ttc gac ccc ggt 144  
 Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Val Thr Phe Asp Pro Gly  
 35 40 45

tat	gtc	agc	acc	ggt	tcc	acc	gaa	tcc	aag	atc	acc	tac	atc	gat	ggt	192	
Tyr	Val	Ser	Thr	Gly	Ser	Thr	Glu	Ser	Lys	Ile	Thr	Tyr	Ile	Asp	Gly		
50				55					60								
gat	gca	ggc	atc	ctg	cgc	tac	cgc	ggc	tac	gac	att	gcg	gat	ctg	gcc	240	
Asp	Ala	Gly	Ile	Leu	Arg	Tyr	Arg	Gly	Tyr	Asp	Ile	Ala	Asp	Leu	Ala		
65				70					75					80			
gaa	aat	gcc	acc	tcc	aat	gag	gtc	tcc	tac	ctc	ctg	atc	aag	ggt	gag	288	
Glu	Asn	Ala	Thr	Phe	Asn	Glu	Val	Ser	Tyr	Leu	Leu	Ile	Lys	Gly	Glu		
				85					90				95				
ctc	ccg	acc	ccg	gaa	gag	ctc	cac	aag	ttc	aac	gac	gag	att	cgt	cac	336	
Leu	Pro	Thr	Pro	Glu	Glu	Leu	His	Lys	Phe	Asn	Asp	Glu	Ile	Arg	His		
				100				105				110					
cac	acc	ctg	ctg	gac	gag	gac	ttc	aag	tcc	cag	ttc	aat	gtc	ttc	cct	384	
His	Thr	Leu	Leu	Asp	Glu	Asp	Phe	Lys	Ser	Gln	Phe	Asn	Val	Phe	Pro		
				115				120				125					
cgc	gat	gcc	cac	ccg	atg	gcc	acc	ctg	gcc	tcc	tcg	gtt	aac	atc	ctc	432	
Arg	Asp	Ala	His	Pro	Met	Ala	Thr	Leu	Ala	Ser	Ser	Val	Asn	Ile	Leu		
				130				135			140						
tcc	acc	tac	tac	cag	gat	cag	ctg	gat	ccc	ctg	gat	gag	gct	cag	ctg	480	
Ser	Thr	Tyr	Tyr	Gln	Asp	Gln	Leu	Asp	Pro	Leu	Asp	Glu	Ala	Gln	Leu		
				145				150			155			160			
gac	aag	gca	acc	gtc	cgc	ctg	atg	gcg	aag	gtt	ccg	atg	ctg	gct	gca	528	
Asp	Lys	Ala	Thr	Val	Arg	Leu	Met	Ala	Lys	Val	Pro	Met	Leu	Ala	Ala		
				165				170			175						
tac	gca	cac	cgt	gcc	cgc	aag	ggt	gcg	ccg	tac	atg	tac	ccg	gac	aac	576	
Tyr	Ala	His	Arg	Ala	Arg	Lys	Gly	Ala	Pro	Tyr	Met	Tyr	Pro	Asp	Asn		
				180				185			190						
tcc	ctc	aat	gcc	cgt	gag	aac	ttc	ctg	cgc	atg	atg	ttc	ggt	tac	ccg	624	
Ser	Leu	Asn	Ala	Arg	Glu	Asn	Phe	Leu	Arg	Met	Met	Phe	Gly	Tyr	Pro		
				195				200			205						
acc	gag	ccg	tac	gag	gtt	gat	ccg	atc	atg	gtc	aaa	gcc	ctc	gac	aag	672	
Thr	Glu	Pro	Tyr	Glu	Val	Asp	Pro	Ile	Met	Val	Lys	Ala	Leu	Asp	Lys		
				210				215			220						
ctg	ctc	atc	ctg	cac	gca	gac	cac	gag	cag	aac	tgc	tcc	acc	tcc	act	720	
Leu	Leu	Ile	Leu	His	Ala	Asp	His	Glu	Gln	Asn	Cys	Ser	Thr	Ser	Thr		
				225				230			235			240			
gtc	cgc	atg	atc	ggc	tcc	gcg	cag	gcg	aac	atg	ttc	gtc	tcc	atc	gcc	768	
Val	Arg	Met	Ile	Gly	Ser	Ala	Gln	Ala	Asn	Met	Phe	Val	Ser	Ile	Ala		
				245				250			255						
ggc	ggc	atc	aac	gca	ctc	tcc	ggc	ccg	ctg	cac	ggt	ggc	gcc	aac	cag	816	
Gly	Gly	Ile	Asn	Ala	Leu	Ser	Gly	Pro	Leu	His	Gly	Gly	Ala	Asn	Gln		
				260				265			270						
gct	gtc	ctc	gag	atg	ctc	gag	gag	atc	gca	gcc	aac	ggc	ggc	gac	gca	864	
Ala	Val	Leu	Glu	Met	Leu	Glu	Glu	Ile	Ala	Ala	Asn	Gly	Gly	Asp	Ala		
				275				280			285						
acc	gac	tcc	atg	aac	cgc	gtg	aag	aac	aag	gag	aag	ggt	gtc	cgc	ctc	912	
Thr	Asp	Phe	Met	Asn	Arg	Val	Lys	Asn	Lys	Glu	Lys	Gly	Gly	Val	Arg	Leu	
				290				295			300						
atg	ggc	tcc	gga	cac	cgc	gtc	tac	aag	aac	tac	gat	ccg	cgt	gca	gcc	960	
Met	Gly	Phe	Gly	His	Arg	Val	Tyr	Lys	Asn	Tyr	Asp	Pro	Arg	Ala	Ala		
				305				310			315			320			

atc gtc aag gac acc gcc cac gag atc ctc gag cac ctc ggt ggc gac	1008
Ile Val Lys Asp Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp	
325 330 335	
cca ctg ctg gat ctg gct ctc aag ctg gaa gaa atc gca ctc aac gac	1056
Pro Leu Leu Asp Leu Ala Leu Lys Leu Glu Glu Ile Ala Leu Asn Asp	
340 345 350	
gat tac ttc atc tcc cgc aag ctg tac ccg aac gtg gac ttc tac acc	1104
Asp Tyr Phe Ile Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr	
355 360 365	
ggc ctg atc tac cgc gcc atg ggc ttc ccg acg gac ttc ttc acc gtc	1152
Gly Leu Ile Tyr Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val	
370 375 380	
ctg ttc gcc atc ggc cgc ctc ccg ggc tgg atc gcc cac tac cgc gag	1200
Leu Phe Ala Ile Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu	
385 390 395 400	
cag ctc gcc gat ccg ggc gcc aag atc aac cgt cct cgc cag atc tac	1248
Gln Leu Ala Asp Pro Gly Ala Lys Ile Asn Arg Pro Arg Gln Ile Tyr	
405 410 415	
acc ggt gag acc gca cgc aag atc atc ccc cgc gaa gag cgc tag	1293
Thr Gly Glu Thr Ala Arg Lys Ile Ile Pro Arg Glu Glu Arg	
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<210> 90

<211> 430

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 90

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Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Val Thr Phe Asp Pro Gly	
35 40 45	
Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly	
50 55 60	
Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala	
65 70 75 80	
Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Lys Gly Glu	
85 90 95	
Leu Pro Thr Pro Glu Glu Leu His Lys Phe Asn Asp Glu Ile Arg His	
100 105 110	
His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro	
115 120 125	
Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu	
130 135 140	
Ser Thr Tyr Tyr Gln Asp Gln Leu Asp Pro Leu Asp Glu Ala Gln Leu	
145 150 155 160	
Asp Lys Ala Thr Val Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala	
165 170 175	
Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn	

	180	185	190												
Ser	Leu	Asn	Ala	Arg	Glu	Asn	Phe	Leu	Arg	Met	Met	Phe	Gly	Tyr	Pro
	195						200					205			
Thr	Glu	Pro	Tyr	Glu	Val	Asp	Pro	Ile	Met	Val	Lys	Ala	Leu	Asp	Lys
	210						215					220			
Leu	Leu	Ile	Leu	His	Ala	Asp	His	Glu	Gln	Asn	Cys	Ser	Thr	Ser	Thr
	225						230					235			240
Val	Arg	Met	Ile	Gly	Ser	Ala	Gln	Ala	Asn	Met	Phe	Val	Ser	Ile	Ala
	245						250								255
Gly	Gly	Ile	Asn	Ala	Leu	Ser	Gly	Pro	Leu	His	Gly	Gly	Ala	Asn	Gln
	260						265					270			
Ala	Val	Leu	Glu	Met	Leu	Glu	Glu	Ile	Ala	Ala	Asn	Gly	Gly	Asp	Ala
	275						280					285			
Thr	Asp	Phe	Met	Asn	Arg	Val	Lys	Asn	Lys	Glu	Lys	Gly	Val	Arg	Leu
	290						295					300			
Met	Gly	Phe	Gly	His	Arg	Val	Tyr	Lys	Asn	Tyr	Asp	Pro	Arg	Ala	Ala
	305						310					315			320
Ile	Val	Lys	Asp	Thr	Ala	His	Glu	Ile	Leu	Glu	His	Leu	Gly	Gly	Asp
	325						330						335		
Pro	Leu	Leu	Asp	Leu	Ala	Leu	Lys	Leu	Glu	Glu	Ile	Ala	Leu	Asn	Asp
	340						345						350		
Asp	Tyr	Phe	Ile	Ser	Arg	Lys	Leu	Tyr	Pro	Asn	Val	Asp	Phe	Tyr	Thr
	355						360					365			
Gly	Leu	Ile	Tyr	Arg	Ala	Met	Gly	Phe	Pro	Thr	Asp	Phe	Phe	Thr	Val
	370						375					380			
Leu	Phe	Ala	Ile	Gly	Arg	Leu	Pro	Gly	Trp	Ile	Ala	His	Tyr	Arg	Glu
	385						390					395			400
Gln	Leu	Ala	Asp	Pro	Gly	Ala	Lys	Ile	Asn	Arg	Pro	Arg	Gln	Ile	Tyr
	405						410						415		
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<211> 1314

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1)..(1311)

<400> 91

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Met	Phe	Glu	Arg	Asp	Ile	Val	Ala	Thr	Asp	Asn	Asn	Lys	Ala	Val	Leu	
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1					5				10					15	
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cac	tac	ccc	ggt	ggc	gag	ttc	gaa	atg	gac	atc	atc	gag	gct	tct	gag	96
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His	Tyr	Pro	Gly	Gly	Glu	Phe	Glu	Met	Asp	Ile	Ile	Glu	Ala	Ser	Glu	
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20					25					30					
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ggt	aac	aac	ggt	gtt	gtc	ctg	ggc	aag	atg	ctg	tct	gag	act	gga	ctg	144
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Gly	Asn	Asn	Gly	Val	Val	Leu	Gly	Lys	Met	Leu	Ser	Glu	Thr	Gly	Leu	
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35					40					45					
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atc	act	ttt	gac	cca	ggt	tat	gtg	agc	act	ggc	tcc	acc	gag	tcg	aag	192
Ile	Thr	Phe	Asp	Pro	Gly	Tyr	Val	Ser	Thr	Gly	Ser	Thr	Glu	Ser	Lys	
50							55					60				
atc	acc	tac	atc	gat	ggc	gat	gcf	gga	atc	ctg	cgt	tac	cgc	ggc	tat	240
Ile	Thr	Tyr	Ile	Asp	Gly	Asp	Ala	Gly	Ile	Leu	Arg	Tyr	Arg	Gly	Tyr	
65							70				75			80		
gac	atc	gct	gat	ctg	gct	gag	aat	gcc	acc	ttc	aac	gag	gtt	tct	tac	288
Asp	Ile	Ala	Asp	Leu	Ala	Glu	Asn	Ala	Thr	Phe	Asn	Glu	Val	Ser	Tyr	
							85				90			95		
cta	ctt	atc	aac	ggt	gaa	cta	cca	acc	cca	gat	gag	ctt	cac	aag	ttt	336
Leu	Leu	Ile	Asn	Gly	Glu	Leu	Pro	Thr	Pro	Asp	Glu	Leu	His	Lys	Phe	
							100				105			110		
aac	gac	gag	att	cgc	cac	cac	acc	ctt	ctg	gac	gag	gac	ttc	aag	tcc	384
Asn	Asp	Glu	Ile	Arg	His	His	Thr	Leu	Leu	Asp	Glu	Asp	Phe	Lys	Ser	
							115				120			125		
cag	ttc	aac	gtg	tcc	cca	cgc	gac	gct	cac	cca	atg	gca	acc	ttg	gct	432
Gln	Phe	Asn	Val	Phe	Pro	Arg	Asp	Ala	His	Pro	Met	Ala	Thr	Leu	Ala	
							130				135			140		
tcc	tcg	gtt	aac	att	ttg	tct	acc	tac	tac	cag	gat	cag	ctg	aac	cca	480
Ser	Ser	Val	Asn	Ile	Leu	Ser	Thr	Tyr	Tyr	Gln	Asp	Gln	Leu	Asn	Pro	
							145				150			155		160
ctc	gat	gag	gca	cag	ctt	gat	aag	gca	acc	gtt	cgc	ctc	atg	gca	aag	528
Leu	Asp	Glu	Ala	Gln	Leu	Asp	Lys	Ala	Thr	Val	Arg	Ieu	Met	Ala	Lys	
							165				170			175		
gtt	cca	atg	ctg	gct	gcf	tac	gca	cac	cgc	gca	cgc	aag	ggt	gct	cct	576
Val	Pro	Met	Leu	Ala	Ala	Tyr	Ala	His	Arg	Ala	Arg	Lys	Gly	Ala	Pro	
							180				185			190		
tac	atg	tac	cca	gac	aac	tcc	ctc	acc	gcf	cgt	gag	aac	ttc	ctg	cgc	624
Tyr	Met	Tyr	Pro	Asp	Asn	Ser	Leu	Asn	Ala	Arg	Glu	Asn	Phe	Leu	Arg	
							195				200			205		
atg	atg	tcc	ggt	tac	cca	acc	gag	cca	tac	gag	atc	gac	cca	atc	atg	672
Met	Met	Phe	Gly	Tyr	Pro	Thr	Glu	Pro	Tyr	Glu	Ile	Asp	Pro	Ile	Met	
							210				215			220		
gtc	aag	gct	ctg	gac	aag	ctg	ctc	atc	ctg	cac	gct	gac	cac	gag	cag	720
Val	Lys	Ala	Leu	Asp	Lys	Leu	Leu	Ile	Leu	His	Ala	Asp	His	Glu	Gln	
							225				230			235		240
aac	tgc	tcc	acc	tcc	acc	gtt	cgt	atg	atc	ggt	tcc	gca	cag	gcc	aac	768
Asn	Cys	Ser	Thr	Ser	Thr	Val	Arg	Met	Ile	Gly	Ser	Ala	Gln	Ala	Asn	
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atg	ttt	gtc	tcc	atc	gct	ggt	ggc	atc	acc	gct	ctg	tcc	ggc	cca	ctg	816
Met	Phe	Val	Ser	Ile	Ala	Gly	Gly	Ile	Asn	Ala	Leu	Ser	Gly	Pro	Leu	
							260				265			270		
cac	ggt	ggc	gca	aac	cag	gct	gtt	ctg	gag	atg	ctc	gaa	gac	atc	aag	864
His	Gly	Gly	Ala	Asn	Gln	Ala	Val	Leu	Glu	Met	Leu	Glu	Asp	Ile	Lys	
							275				280			285		
aac	aac	cac	ggt	ggc	gac	gca	acc	gcf	ttc	atg	aac	aag	gtc	aag	aac	912
Asn	Asn	His	Gly	Gly	Asp	Ala	Thr	Ala	Phe	Met	Asn	Lys	Val	Lys	Asn	
							290				295			300		
aag	gaa	gac	ggc	gtc	cgc	ctc	atg	ggc	ttc	gga	cac	cgc	gtt	tac	aag	960
Lys	Glu	Asp	Gly	Val	Arg	Leu	Met	Gly	Phe	Gly	His	Arg	Val	Tyr	Lys	
							305				310			315		320

aac tac gat cca cgt gca gca atc gtc aag gag acc gca cac gag atc	1008
Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu Thr Ala His Glu Ile	
325 330 335	
ctc gag cac ctc ggt ggc gac gat ctt ctg gat ctg gca atc aag ctg	1056
Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu	
340 345 350	
gaa gaa att gca ctg gct gat gat tac ttc atc tcc cgc aag ctc tac	1104
Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr	
355 360 365	
ccg aac gta gac ttc tac acc ggc ctg atc tac cgc gca atg ggc ttc	1152
Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe	
370 375 380	
cca act gac ttc ttc acc gta ttg ttc gca atc ggt cgt ctg cca gga	1200
Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile Gly Arg Leu Pro Gly	
385 390 395 400	
tgg atc gct cac tac cgc gag cag ctc ggt gca gca ggc aac aag atc	1248
Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala Ala Gly Asn Lys Ile	
405 410 415	
aac cgc cca cgc cag gtc tac acc ggc aag gaa tcc cgc aag ttg gtt	1296
Asn Arg Pro Arg Gln Val Tyr Thr Gly Lys Glu Ser Arg Lys Leu Val	
420 425 430	
cct cgc gag gag cgc taa	1314
Pro Arg Glu Glu Arg	
435	

<210> 92  
 <211> 437  
 <212> PRT  
 <213> Brevibacterium lactofermentum

<400> 92	
Met Phe Glu Arg Asp Ile Val Ala Thr Asp Asn Asn Lys Ala Val Leu	
1 5 10 15	
His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile Ile Glu Ala Ser Glu	
20 25 30	
Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu Ser Glu Thr Gly Leu	
35 40 45	
Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys	
50 55 60	
Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr	
65 70 75 80	
Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr	
85 90 95	
Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp Glu Leu His Lys Phe	
100 105 110	
Asn Asp Glu Ile Arg His His Thr Leu Leu Asp Glu Asp Phe Lys Ser	
115 120 125	
Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro Met Ala Thr Leu Ala	
130 135 140	
Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro	
145 150 155 160	

Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val Arg Leu Met Ala Lys  
                  165                 170                 175  
 Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala Arg Lys Gly Ala Pro  
                  180                 185                 190  
 Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg  
                  195                 200                 205  
 Met Met Phe Gly Tyr Pro Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met  
                  210                 215                 220  
 Val Lys Ala Leu Asp Lys Leu Ile Leu His Ala Asp His Glu Gln  
                  225                 230                 235                 240  
 Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly Ser Ala Gln Ala Asn  
                  245                 250                 255  
 Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu  
                  260                 265                 270  
 His Gly Gly Ala Asn Gln Ala Val Leu Glu Met Leu Glu Asp Ile Lys  
                  275                 280                 285  
 Asn Asn His Gly Gly Asp Ala Thr Ala Phe Met Asn Lys Val Lys Asn  
                  290                 295                 300  
 Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly His Arg Val Tyr Lys  
                  305                 310                 315                 320  
 Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu Thr Ala His Glu Ile  
                  325                 330                 335  
 Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu  
                  340                 345                 350  
 Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr  
                  355                 360                 365  
 Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe  
                  370                 375                 380  
 Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile Gly Arg Leu Pro Gly  
                  385                 390                 395                 400  
 Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala Ala Gly Asn Lys Ile  
                  405                 410                 415  
 Asn Arg Pro Arg Gln Val Tyr Thr Gly Lys Glu Ser Arg Lys Leu Val  
                  420                 425                 430  
 Pro Arg Glu Glu Arg  
                  435

<210> 93  
 <211> 1656  
 <212> DNA  
 <213> Corynebacterium thermoaminogenes

<220>  
 <221> CDS  
 <222> (309)..(1595)

<400> 93  
 acgccccgatt cttcaacact atcgaagagg tcccaaccca cgcgttgacc cagggcttgg 60  
 gtactttgtc ccgcgcgcaa aatatcgtgt tggtgccaaac tggccaagga aaagcagaca 120  
 gccatcccgcg gaactgtgga aggtccagtg actgcttctt gcccaggttc cattctgcaa 180  
 atgcacacaaca acgccaccat catcggtat gaagcagcag catccaagct gaaaaatgct 240

gaccattacc gtctcatgga gcaattaaag ctgcgctaga aacaaaaagg aaagtactgt 300  
 gtggggct atg cac aca gaa ctt tcc agt ttg cgc cct gcg tac cat gtg 350  
 Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val  
 1 5 10  
 act cct ccg cag ggc aga ctc aat gat ccc aat gga atg tac gtc gat 398  
 Thr Pro Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp  
 15 20 25 30  
 gga gat acc ctc cac gtc tac tac cag cac gat cca ggt ttc ccc ttc 446  
 Gly Asp Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe  
 35 40 45  
 gca cca aag cgc acc ggt tgg gct cac acc acc acg ccg ttg acc gga 494  
 Ala Pro Lys Arg Thr Gly Trp Ala His Thr Thr Pro Leu Thr Gly  
 50 55 60  
 ccg cag cga ttg cag tgg acg cac ctg ccc gat gct ctt tac ccg gat 542  
 Pro Gln Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp  
 65 70 75  
 gta tcc tat gac ctg gat gga tgc tat tcc ggc gga gcc gta ttt tct 590  
 Val Ser Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser  
 80 85 90  
 gac ggc acg ctt aaa ctt ttc tac acc ggc aac cga aaa att gac ggc 638  
 Asp Gly Thr Leu Lys Leu Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly  
 95 100 105 110  
 aag cgc cgc gcc acc caa aac ctc gtc gaa gtc gag gac cca act ggg 686  
 Lys Arg Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly  
 115 120 125  
 ctg atg ggc ggc att cat cgc cgc tcg cct aaa aat ccg ctt atc gac 734  
 Leu Met Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp  
 130 135 140  
 gga ccc gcc agc ggt ttt acg ccc cac tac cgc gat ccc atg atc agc 782  
 Gly Pro Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser  
 145 150 155  
 cct gat ggg gat ggt tgg aag atg gtt ctt ggg gct cag cgc gaa aac 830  
 Pro Asp Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn  
 160 165 170  
 ctc acc ggt gca gcg gtt cta tac cgc tcg gca gat ctt gaa aac tgg 878  
 Leu Thr Gly Ala Ala Val Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp  
 175 180 185 190  
 gaa ttc tcc ggt gaa atc acc ttt gac ctc agc gac gca caa cct ggt 926  
 Glu Phe Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly  
 195 200 205  
 tct gcc cct gat ctc gtt cct ggc ggc tac atg tgg gaa tgc ccc aac 974  
 Ser Ala Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn  
 210 215 220  
 ctt ttt acg ctt cgc gat gaa aaa acc ggc gaa gac ctc gat gtg ctg 1022  
 Leu Phe Thr Leu Arg Asp Glu Lys Thr Gly Glu Asp Leu Asp Val Leu  
 225 230 235  
 att ttc tgt cca caa gga ttg gac cgt atc gat gat gag gtt act cac 1070  
 Ile Phe Cys Pro Gln Gly Leu Asp Arg Ile Asp Asp Glu Val Thr His  
 240 245 250  
 tac gca agc tct gac cag tgc gga tat gtc gtc ggc aag ctt gaa gaa 1118  
 Tyr Ala Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Glu

255	260	265	270	
acg acc ttc cgt gtc ctg cga gga ttc agc gag ctg gat ttc ggt cat				1166
Thr Thr Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His				
275	280	285		
gaa ttc tac gcg ccg cag gtt gca gtc aac ggt tcc gat gcc tgg ctt				1214
Glu Phe Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu				
290	295	300		
gtg ggc tgg atg gga ttg cct gca cag gat gat cac cca aca gtt gcg				1262
Val Gly Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala				
305	310	315		
cag gaa gga tgg gtg cac tgc ctg acc gtt cct cgc agg ctt cat ttg				1310
Gln Glu Gly Trp Val His Cys Leu Thr Val Pro Arg Arg Leu His Leu				
320	325	330		
cgt aac cat gcg atc tat caa gag ctt ctt ctc cca gaa ggg gag tcg				1358
Arg Asn His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser				
335	340	345	350	
ggg gta act aga tct gta tta ggt tct gaa cct gtc cga gta gac atc				1406
Gly Val Thr Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile				
355	360	365		
cga gac aat gtt tcc ctc gag tgg gat ggt gtc cgg ttg tct gtg gat				1454
Arg Asp Asn Val Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp				
370	375	380		
cgc gat ggc gat cgt cgt gta gct gaa gta aaa cct ggc gaa tta gtg				1502
Arg Asp Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val				
385	390	395		
atc gcg gac gat aat aca gcg att gag ata aca gca ggt cat ggc cag				1550
Ile Ala Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly His Gly Gln				
400	405	410		
gtt tcc ttc gct ttc cgc acc ttc aaa ggt gac act att gag aga				1595
Val Ser Phe Ala Phe Arg Thr Phe Lys Gly Asp Thr Ile Glu Arg				
415	420	425		
taagtcataa aaaagggcct tctgtggcgg attgtacaaa tacttcgcaa aatcccttga				1655
t				1656

<210> 94  
 <211> 429  
 <212> PRT  
 <213> Corynebacterium thermoaminogenes

1	5	10	15	
Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp	20	25	30	
Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro	35	40	45	
Lys Arg Thr Gly Trp Ala His Thr Thr Pro Leu Thr Gly Pro Gln	50	55	60	
Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser	65	70	75	80
Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly				

85	90	95
Thr Leu Lys Leu Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly Lys Arg		
100	105	110
Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met		
115	120	125
Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro		
130	135	140
Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp		
145	150	155
Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr		
165	170	175
Gly Ala Ala Val Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp Glu Phe		
180	185	190
Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala		
195	200	205
Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe		
210	215	220
Thr Leu Arg Asp Glu Lys Thr Gly Glu Asp Leu Asp Val Leu Ile Phe		
225	230	235
Cys Pro Gln Gly Leu Asp Arg Ile Asp Asp Glu Val Thr His Tyr Ala		
245	250	255
Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Glu Thr Thr		
260	265	270
Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe		
275	280	285
Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly		
290	295	300
Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala Gln Glu		
305	310	315
Gly Trp Val His Cys Leu Thr Val Pro Arg Arg Leu His Leu Arg Asn		
325	330	335
His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val		
340	345	350
Thr Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile Arg Asp		
355	360	365
Asn Val Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp Arg Asp		
370	375	380
Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala		
385	390	395
Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly His Gly Gln Val Ser		
405	410	415
Phe Ala Phe Arg Thr Phe Lys Gly Asp Thr Ile Glu Arg		
420	425	

<210> 95

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for amplifying scrB gene

<400> 95  
gtacatattg tcgttagaac gcgtaatacg actca 35

<210> 96  
<211> 35  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for amplifying scrB gene

<400> 96  
cgtagaaacg cgtaatacga ctcactatag ggaga 35

<210> 97  
<211> 30  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for LA cloning of scrB

<400> 97  
gtaaagagcg tcgggcaggt gcgtccactg 30

<210> 98  
<211> 30  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for LA cloning of scrB

<400> 98  
ggtgtgagcc cagccgggtgc gctttgggtgc 30

<210> 99  
<211> 30  
<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for  
LA cloning of scrB

<400> 99  
atcagccctg atgggtatgg ttggaaaatg 30

<210> 100  
<211> 30  
<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for  
LA cloning of scrB gene

<400> 100  
ggtgcaagcgg ttctataccg ctcgacagat 30

<210> 101  
<211> 32  
<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for  
amplifying scrB gene

<400> 101  
ggcccgggac gcccgattct tcaacactat cg 32

<210> 102  
<211> 32  
<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for  
amplifying scrB gene

<400> 102  
ggcccgggga tcaaggatt ttgcgaagta tt 32

<210> 103  
<211> 30  
<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for  
amplifying icd gene

<400> 103  
gaagatctct atgaccagcg catcaagctg 30

<210> 104  
<211> 30  
<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for  
amplifying icd gene

<400> 104  
gaagatctgg tcatcccaga acctgatcac 30

<210> 105  
<211> 32  
<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for  
amplifying gdh gene

<400> 105  
gcgcctgcag gtccgagggt gtgcgttcgg ca 32

<210> 106  
<211> 32  
<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for  
amplifying gdh gene

<400> 106  
gcgcctgcag gcaccaggat gccctcaacc ag 32

<210> 107  
<211> 30  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for  
amplifying gltA gene

<400> 107

gggttaccga tcactataac cccacagcac

30

<210> 108

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for  
amplifying gltA gene

<400> 108

gggttaccct ggctgatctg aactaggcgc

30